65 υ May 25, 2004, 13:43:01; Search time 3357 Seconds (without alignments) 6029.549 Million cell updates/sec 1 caatgitigoctatccacct......taataaacagitaaaagcig 467 6940544 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 3470272 segs, 21671516995 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 1: 9b ba: *
2: 9b htg: *
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4: 9b om: *
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7: 9b pat: *
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10: 9b pr: *
11: 9b pr: SEQ29-NA-TRUNCATED Minimum DB seq length: 0 Maximum DB seq length: 2000000000 GenEmbl:* Scoring table: Title: Perfect score: Database : Sequence: Searched: Run on:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		AX092298 Sequence	omo sap	BC021104 Homo sapi	equen	uman	omo sa	rimer f	Omo	ednence	equer	eguer	rimer	attus	Mus mu	Mouse	Mous	fomo san	equence	equenc	AX344561 Sequence	attus	AC105482 Rattus no	fus mus	ACII9515 RACTUS NO	Mouse	an tro	er Ver	AL121911 Human DNA	ĮÖ,	למל Sat	onse o	M20136 Mouse beta- M76700 Drosophila	Mouse	Rattu	AE000663 Mus muscu	Mus mus	Ошон	AC122805 Mus muscu	Rattus	Rattus	Homo s	Datting	AC097301 Rattus no	Rattus	Kattus Rattus	Ношов	Zebraf	ion (RATTUS	Rattus	Ctenop
SUMMARIES		AX092298	AX696953	A1556657 BC021104	AR211704	HS454M7	AF195953	AX877684	BUID6/91	ANULGOO	AX332852	AX874329	BD154391	AC127934	AC136814 R/020015	AL714010	AL672274	AC055817	HUMZD38F03	AX344562	AX344561	AC116367	AC105482	AC101159	AC119515	AC107465 AL606973	AC146436	AF441245	AC133581 HSDJ989D7	AC093112	AC114853	MUSTCBVC	MUSTCRBBA	DROZSTA AT.603889	AC128156	MMAE000663	AC125228 AC124343	AC091992	AC122805	AC131668 AC125852	AC120601	AC007597	AC007610	AC103418 AC097301	AC117339	AC103283	AC096336 AP005854	BX004795	AC105872_2	AC005177	AC126834	AY225852
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Color	CTGCTGCTGCTGCTGCTTAAAGGCTCATGGAGGGGGACTGGTGGGTG	NURSHALES ORGANISM Homo sapiens Bucharyota, Mamalia; Putharia; Primates; Catarrhin; Hominidae; Homo. Bucharyota, Mamalia; Dutheria; Primates; Catarrhin; Hominidae; Homo. Godowski, P.J., Gurney, A.L., Smith, V., Tennas, D., Wood, W.L., Grimalid; C.J., Hillan, K.J., Panni, N.F., Roy, M.A. and Waranabe, C.K. TITLE Secreted and transmembrane polypeptides and nucleic acids encoding JOURNAL Genentech Inc. (US) FRATURES Location/Qualifiers Location/Qualifiers Jorganism=Himom sapiens" Anol_type="unassigned DNa" Aboref="text-aron; 960" Watches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OY CTGCTGCTGCTGCTGCTCCCCCAAGCCCTTACCTATGCTGCTAACGCTGCTG OY CTGCTATCCTATCCTATCCCTATCCCTATGCTTAACGTGCTGAAAA120 CTGCTGCTGCTGCTGCTGCTGCTGCTGAAGGCCCTTTACCTATGCTGCTAAAA120 OY CTGCTATCTATCTGCTAATCCACTCCCCCAAGGCCCTTTACCTTAAGGTGCTGCAAAA120 OY CTGCTATCTATCTGCTAATCCACTCCCCCAAGGCCCTTTACCTTAAGGTGCTGCAAAA120 OY CTGCTACTGCTGCTGCTGCTGCTAATGCTTGCAGGGGCTTCTTTTTTTG 180 CTGCTGCTGCTGCTGCTGCTAAAGGCTCATTACTTGCAGGGGCTTTACTTTTTTTT
eso → R R R R R R R R R R R R R R R R R R	8.9 190402 2 ACI14715 ACI14715 ACI33028 8.8 61020 6 AX251545 ACI22951 8.8 174423 2 ACI22951 8.8 174423 2 ACI22951 8.8 174423 2 ACI22951 8.8 190024 2 ACI32595 ACI32951 8.8 179642 2 ACI3245 ACI32006 8.8 179642 2 ACI3245 ACI3245 ACI3246 ACI3246 ACI3246 8.8 179642 2 ACI3246 ACI32318 8.7 570357 2 ACI3242 ACI32318 8.7 570357 2 ACI32331 ACI3242 ACI32331 8.7 125020 9 AC423315 ACI32331 A	ALIGNMENTS AX092298 AX092298 AX092298.1 GI:13444463 Homo sapiens (human) Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Eutel Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo Eaton, D. L., Filvaroff, E., Gerritsen, M.E., Goddard, A., Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids the same Patent: WO 116318-A 29 08-MAR-2001; Genentech, Inc. (US) Genetech, Inc. (US) I344 Amol type="unassigned DNA" / Mol type="unassigned DNA" / Mol type="unassigned DNA" / Ab_xref="taxon:9606" / Mol xref="taxon:9606" / Ab_xref="taxon:9606" / Ab_xref="taxon:9606" / Ab xref="taxon:9606" / Ab xref="taxon

2488 GGCTAGGGGGCTGCCTTATTTAAAGTGGTTGTTATGATTCTTATACTAATTTATACAA 2547 PAT 20-JUN-2002 1459 ó 1398 Greterrendededededededentadadarradaderrinedederrendedentada 1339 1338 Tércrécrédécrédecrédécardacerdedecradeceadecedecedes 1279 1219 1158 AGATATTAAGGCCCCGGTCATTAAGAAATTGTTCCCCTTCCCCTGTGTTCAATGTTTGTAA 1099 241 GAGAAAGTGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTG 300 61 CIGCIGCIGCIGCITAAAGGCICATGCTIGGAGIGGGGACIGGICGGIGCCCAGAAA 120 240 300 420 1518 CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTG GGCTAGGGGGCTGCCTTATTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAA AGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAA 1 CAAIGITIGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTG 1458 CTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGGACTGGTCGGTGCCCAGAAA TGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCCAGCCCCGTGGGGAAGGG 1278 GAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAAACAGAAGAGGGTAGTGGGTG AGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAA 241 GAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAAGATAGGGAACAGAAGAGGGGTAGTAGTG GGCTAGGGGGGCTGCCTTATTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAA Gaps 0; Length 50000; 2654 AGATIGITCIGIGIAAAIAIGICITIAIAAAAAAAGGITAAAAGCIG 467 AGAITGITCTGTAAATATGTCTTTATAATAAAAGAGTTAAAAGCTG 467 2608 AGATTGTTCTGTGTAATATGTCTTTATAATAAAAGCTG linear 0; Indels 1098 AGATTGTTCTGTGTATATATATAATAAACAGTTAAAAGCTG 100.0%; Score 467; DB 6; I 100.0%; Pred. No. 6.4e-113; ive 0; Mismatches 0; M Unknown.
Unclassified.
3 (bases 1 to 50000)
S Ryam, J.W. and Sprinkle, T. Joe. Curtis.
Human aminopeptidase P gene
AL Patent: US 639349-A 4 04-UNN-2002;
Location/Qualifiers
Location/Qualifiers DNA 1. .50000 /organism="unknown" /mol_type="unassigned DNA" AR211704 50000 bp Seguence 4 from patent US 6399349. GI:21515097 467; Conservative AR211704 AR211704.1 Similarity . Unknown. 30I 361 421 121 181 301 361 421 Query Match Best Local Matches 46 AR211704/c LOCUS DEFINITION ACCESSION VERSION source ORGANISM AUTHORS TITLE

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REFERENCE AUTHORS TITLE

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FHIGWARDERSYRRKVERDSYRRANDFLESLEIGSREFFYERWYRFRQUGKERFY
ISNNGQVPCHFSFIPKLNDSQYCKPWLRAEPFEGYLEPNETVDISLDVYVSKDGVFUL
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32328. .32455,33287. .33398,33588. .33712)
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PROKOSSWYQKLDTKOKPSVFSGLLGFEDNRSSMNLDKKTISSQNQPTGIHREPPPPP
SUNKALPREKEASNKEQFKVTWTMRKL-VPWTQSGQREGLIKHTLAKREKEVVNIQTF
SVRVATWWWKQSPPSGLEPPALNCDPWPPDIYCIGFQELDLSTEAFFYFESVKEQEWS
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FILPTYKYDSKTDRMDSSGKCRVPAMCDRILMRGTNVNQLNYRSHMELKTSDHKPUSAL
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EQKDSSSWYQKLDTKDKPSVFSGLLGPEDNESSWNLDKKINSQVQFGIHREPPPPP
EQKDSSSWYQKLDTKDKPSVFSGLLGPEDNESSWNLDKKINSQVQFGIHREPPPPPP
EQKDSSSWYQKLDTKDFKPVTWTWTLTPVPTQSGQREGIKHILAKREKEYWNIQTP
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FILGVKVVDERRYRKVFEDSVRIMDRMENDFLPSLEILSRREFVFENVKERQLGVKEKFQ
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NSGEDKIEDILVLHLDRGKDYFLTISGNYLPSCFGYSLEALCRWKRFIREVPYTKLID
LEKSLLQWVPLDEGASERPLQVPKEHISGNYLLPSCFGYSLEALCRWKRFIREVPYTKLID
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/note="AluJb repeat: matches 1. .302 of consensus"
6639. .6933
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/note="MIR repeat: matches 2. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not experimental
product="4dJ5EANT.1.2" (variant 2)"
protein id="CAA18150.1"
/db_xref="GI:3171882"
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note="variant 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least on planeing subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em.: EMBL: Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at the WORMPEP database can be found at the WORMPEP database can be found at the worm and accession of the worm part of bacterial clone contigs of human was generated from part of bacterial clone contigs of human was senerated.
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3992. .4093,4621. .4735,5826. .5342,6041. .6228,9214. .9325,
10696. .10805,12706. .12841,18582. .18692,19339. .19504,
19759. .19994,30444. .30560,31621. .31705,3228. .32455,
33287. .33398,33588. .35998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 151152)
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/product="dJ454M7.1.1 (Lowe Oculocerebrorenal Syndrome)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 2, 1998 this sequence version replaced gi:2969945.
                                                                                         HS454M7 151152 bp DNA linear PRI 05-JUN-2 Human DNA sequence from clone RP3-454M7 on chromosome Xq25-26.3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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767. .35998
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                                                                                                                                                                                                                                                                                                                    AL022162.1 GI:3171881
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                  RESULT 6
HS454M7/c
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FEATURES

mRNA

Qy 181 TGTCTCCTGCCTCATCGGCCTGC Db 89538 TGTCTCCTGCCTCATCGGCCTGC Qy 241 GAGAAAGTGGGGGATGGCTAAGA Db 89478 GAGAAAGTGGGGGATGGCTAAGAA	Oy 301 GGCTAGGGGGCTGCCTTATTTA 	RESULT 7 AR195953/C LOCUS DEFINITION Home sapiens membrane-boun Complete cds. ACCESSION VERSION REYWORDS SOURCE HOME Sapiens (human) ORGANISM Home sapiens Eukaryota; Metazca; Chorda Mammalia; Eutheria; Primat REFERENCE I (Dases 1 to 206618) TITLE Human membrane-bound amino JOHRMAL Unpublished REFERENCE 2 (Dases 1 to 206618) AUTHORS Ryan, J. W., Jin, L., Horvath AUTHORS Ryan, J. W., Jin, L., Horvath AUTHORS Ryan, J. W., Jin, L., Horvath	Direct Submission Submitted (18-06 Georgia, 1120 15 3 Georgia, 1120 15 Direct Submission Submitted (26-WH Georgia, 1120 15 Sequence, update On Mar 26, 2002 Ce	Join(144189 .1446 150445 .150508,1 152849 .152894 .152849 .152847,1 167342 .157587,1 16736 .166613,16 16736 .166012,17 Jene="XNPEP2" Jene="RNPEP2" Jene="RNP
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                                                                                                                                                                                                                                                               AAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAA 89299
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und aminopeptidase P (XNPEP2) gene,
                                                                         AAAGCTGGGAGATAGGGAACAGAAGAGGGGTAGTGGGTG 300
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CCATGACCTGCAGCCCAAGCCCCGTGGGGAAGGG 240
                                                                                                                                                                                                                                   AAGAAATIGITCCCTTCCCCTGTGTTCAATGTTTGTAA 420
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stes; Catarrhini, Hominidae; Homo.
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151478. 151582,151837. 151923,
155710. 155811,156987. 157068,
158401. 158490,159714. 159823,
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161726 . 161797,164422 . 164482,
16414 . 166518,167248 . 167307,
172845 . 172934,173533 . 176791)
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                                                                                                                                                                                                                                                                                                                                                          Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthessising full-length cDNA and their use Patent: BP 1074617-A 12589 07-FEB-2001; Research Association for Blotechnology (JP)
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                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTGTCTCCTGCCTCGTGCCTGCCATGACCTGCAGCCCAAGCCCCAGCCCCGTGGGGAA
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                                  51098 AGATTGTTGTGTATAAATATGTCTTTATAATAAAAGCTG
          421 AGATTGTTCTGTGTAAATATGTCTTTATAATAAACAGTTAAAAGCTG
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37.2%; Score 454; DB 6; I
al Similarity 99.4%; Pred. No. 1.6e-109;
467; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="unnamed protein product"
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6. 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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1. .2243
                                                                                                                                                                                                                AX877684.1 GI:40032420
                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
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Matches 467; Conserv
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16066. . 160608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTAGGGGGGCTGCCTTATTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative proton shuttle; unclassified site"
161778. .161780
/gene="XNPEP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="divalent metal ligand; metal-binding site"
164435. .164437
/gene="XNPEP2"
/note="divalent metal ligand; metal-binding site"
166473. .166475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="XXPEP2"
/note="divalent metal ligand; metal-binding site"
15728. .176791
/gene="XXPEP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="XNPEEP2"
'note="divalent metal ligand; metal-binding site"
join(167307,167936. .167937)
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  .166518,167248. .167307, .172934,173533. .173727)
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                                                                               'product="membrane-bound aminopeptidase
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al Similarity 100.0%; Score 467; DB 9; I
al Similarity 100.0%; Pred. No. 6.8e-113;
467; Conservative 0; Mismatches 0;
                                                                                                   /protein_id="AAG28480.1"
/db_xref="GI:11066157"
.65754. .165823,166414.
.67936. .168012,172845.
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(bases 1 to 2243)
gai, T. and Otsuki, T.
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                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                       SOURCE
ORGANISM
                                                                                                          DEFINITION
                                                           RESULT 10
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1 (bases I vo. 2243)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Makamatsu,A., Nagai,K. and Otsuki,T. Primar for Synthesizing full-length cDNA and use thereof.

Patent: JP 2002191363-A 11634 09-JUL-2002;
                                          PAT 17-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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KELICHI NAGAI, TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12NS/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
T CDS
Location/Qualifiers
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                         C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                          JP 2002191363-A/11634
09-JUL-2002
28-JUL-2000 JP 2000280990
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1774 CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTACTAACGCTACTG
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                                   BD156791 2243 bp DNA linear PAT I
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97.2%; Score 454; DB 6; DB 8; DB 6; DB 8; DB 6; DB 8; DB 99.4%; Pred. No. 1.66-109; Matches 467; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                               BD156791.1 GI:27862549
                                                                                                JP 2002191363-A/11634.
Homo sapiens (human)
Homo sapiens
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RESULT 9
BD156791
LOCUS
DEFINITION
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PRI 01-AUG-2002
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Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory: 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan, CDNA full insert
construction, Fesarch Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Hellx Research Institute (supported by Japan Key Technology Center
ctc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSATWCSPEGGGMGQGPGREVGGNSAASGPASPIRNPCLSEAGL
RepBSAHPLELLERLCLLERLVESGGLTSIQLSPRTCCSHQWAQLFSPACFPQWRAPGCSL
DDSRSLTRIPVELLGGSLD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Tog'ya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Rakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A.
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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2194 TAAAGATTGTTCTGTGTAAATATGTCTTTATAATAACAGTTAAAAGCTG 2243
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                                                                                                                                                             Homo sapiens cDNA FLJ10993 fis, clone PLACE1002140. AK001855. AK001855.1 GI:7023382 oligo capping; fis (full insert sequence). Homo sapiens (human)
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/clone lib="PLACE1"
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/note="unnamed protein product"
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1. .2243
/organism="Homo sapiens"
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/db_xref="GI:7023383"
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/db_xref="taxon:9606"
/clone="PLACE1002140"
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seq29-na-truncated.rge

Page 9

	PERENCE AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signs gene sets Genes gene determination and therapeutic screening using signs gene sets JOURNAL Avalon Pharmaceuticals (US) Location/Qualifiers 1. 458 //mol_type="unassigned DNA" //db_xref="taxon:9606" Matches 435; Conservative 0; Mismatches 11; Indels 1; Gaps 22 CCCCAAGCCCTTTACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAAA 458 CCCCAAGCCCTTTACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	201 TGCCATGACCTGCACCCCACCCCTGGGGAAGAGAGGGAAGAGTGGGTA 260
Db 1954 CTGTGTCTCCTGCCTCATGGCCTGCCAGGCCCAGCCCAG	RESULT 11 AX332625 /c LOCUGS AX332625 AX332625 Home sapiens (human) SOURCE SOURCE AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AVAION PLEATMAND AVAION PLEATMAND AVAION PLEATMAND AVAION PARTMAND AVAION PA	Db 458 CCCCAAGCCCTTTACCTATGCTTACTACTACTACTACTACTACTACTACTACTACTATACTAC

Sequence 9234 from Patent EP1074617

AX874329.1 GI:40029100

Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamalia, Eutheria; Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 403)

Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Parent: JP 2002191363-A 9234 09-JUL-2002;

HELIX RESEARCH INSTITUTE

OF HOMO Sapiens (human)

PR 2002191363-A/9234 BD154391 403 bp DNA linear PAT 1 Primer for synthesizing full-length cDNA and use thereof. BD154391.1 GI:27860149 SOURCE RESULT 14 BD154391/c LOCUS ACCESSION VERSION KEYWORDS JOURNAL REFERENCE COMMENT

PAT 17-JAN-2003

ó JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI HTG 19-NOV-2002 ပ္ပ 344 184 284 244 364 224 304 164 424 Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Angaliano, D., Allen, C., Allen, H., Alsbrooks, S., Anin, A., Angaliano, D., Anyaleberi, V., Ayorgi, A., Ayodej, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., 163 AGGGGGCTGCCTTATTAAAGTGGTTGTTTATGATTNTTATACTAATTTATACAAAGAT 104 44 PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATI KEIICHI NAGAI, TETSUJI OTSUKI
PC CI2NIS/09, CO7K14/47, CO7K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC (C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 Primer for synthesizing full-length cDNA and use thereof FH K Location/Qualifiers Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 403 TGCTGNTGCTGCTTAAAGGCTCATGNTTGGAGTGGGGANTGGTCGGTGCCAGAAAGTTT 365 ATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGAT 103 ATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCTGTGTTCAATGTTTGTAAAGAT 185 TCCTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGGAGA AGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGAT 343 TTTTTGCCACTGACGCCCCCATCAGGGATTGGGCNTTNTTTCCCCCTTCCTTTNTGTGTC Gaps ACL27934 171310 bp DNA linear HTG 19-NK Rattus norvegicus clone CH230-32806, WORKING DRAFT SEQUENCE. ACL27934 ·. Length 403; 'organism='Homo sapiens (human)' 10; Indels 425 IGTICIGIGIAAATAIGICITITAIAAAAACAGITAAAAGCIG 467 AC127934.3 GI:25075008 HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP. Rattus norvegicus (Norway rat) Rattus norvegicus Score 391.2; DB 6; Pred. No. 7.1e-93; 0; Mismatches 10; 1. .403 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" 1. .403 Location/Qualifiers Query Match 83.8%; Best Local Similarity 97.5%; Matches 393; Conservative source Rattus. FT 305 65 source DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 15 AC127934 REFERENCE AUTHORS FEATURES ORIGIN LOCUS d à ò ΩD g 셤 g à à ð 셤 ð à

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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chardenas, V., Carter, C., Chavazo, I., Charden, S., Chen, Y., Chen, Z., Claveland, C., Cockreal, B., Cox, C., Coyle, M., Cree, A., D'Souza, L. Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C. Dederich, D. Deggado, O., Denson, S., Derman, C., Ding, Y., Dinh, H., Davya, K., Bagar, A., Bacotto, M., Eugene, C., Erans, C.A., Falls, T., Fan, G., Fan, C., Fand, C., Davas, E., Fan, C., Gebregocrafis, E., Gear, K., Garcia, A., Garcia, A., Garcia, M., Gebregocrafis, E., Gear, K., Gill, R., Garcia, A., Garcia, M., Gebregocrafis, E., Gear, K., Gill, R., Garcia, M., Gebregocrafis, E., Gear, K., Gill, R., Garcia, M., Gebregocrafis, E., Gear, K., Hamilton, C., Hamilton, C., Hamilton, K., Harnandez, F., Hadun, S.L., Hodgeson, M., Honlins, B., Hadun, R., Fan, M., Hander, C., Han, F., Handerson, M., Honlins, B., Hadun, R., Tan, M., Mannatarne, M., Mannatarne, M., Mannatarne, M., Mannatarne, M., Martinez, M., Martinez, E., Mannatarne, J., Martinez, E., Mannatarne, M., Mannatarne, M., Martinez, E., Mannatarne, C., Nachod, M., P., Martin, R., Mannatarne, M., Martin, R., Mannatarne, M., Martin, R., Mannatarne, M., Martin, R., Mannatarne, M., Martin, M.
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Nlederhausern,A., Weiss,R.,
Weinstock,G. and Gibbs,R.A.
Unpublished
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Worley, K.C.
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JOURNAL
REFERENCE
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Direct Submission

Submitted (19-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Sat Genome Sequencing Consortium.

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23915370.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgum sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence cortigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature

AUTHORS TITLE JOURNAL

Center: Baylor College of Medicine Center code: BCM Genome Center table. REFERENCE AUTHORS TITLE JOURNAL COMMENT

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116761 TGATTGCCTATTCACCCGTCCCAAAATCCTTCCCATCTGCTGCTGCTAATGCTGCTGCTGC 116820
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                                                                                                                                                                                                                                                                                                  * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 1 contigs. daps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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                                                               4 TGTTTGCCTATCCACCTCCCCCAAGCCCCTTTAACCTATGCTGCTGCTAACGCTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 CIGCIGCIGCIGCTIAAAGGCICAIGCIIGGAGIGGGGACIGGICGGIGCCCAGAAAGIC
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1 171310: contig of 171310 bp in length.
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site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Rattus norvegicus"
                                             Project Information
                         Contact: hgsc-help@bcm.tmc.edu
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clone_end:Sp6"
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Muzny, D. Marie, Metzker, M. Lee, Adramzon, S., Adams, C., Alder, J., Angalano, D., Angalahen, Metzker, M. Lee, Addelji, M., Baca, B., Badden, H., Balanden, Y., Chen, B., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Broan, M., Bryant, N., Edaleron, E., Carderon, E., Carderon, E., Carderon, E., Carderon, E., Carderon, C., Chen, R., Cher, A., D'Souza, L., Clackon, J., Chave, D., Chave, C., Corle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Dermon, C., Dinh, H., Divya, K., Drapar, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Escotto, M., Engen, C., Evalla, K., Carde, M., Diagan, A., Ealla, T., Fan, G., Fernandez, S., Finley, M., Fagg, M., Forbes, L., Foster, M., Gener, P., Fraser, C.M., Gabe, S., Mulyk, S., Hadan, W., Hamil, Co., A., Garrar, M., Gurara, M., Gunzar, M., Gunza, M., Garze, M., Handle, C., Hamilton, K., Harandez, P., Hadan, W., Hamil, C., Hamilton, K., Harandez, R., Hines, S., Hald, M., S., Kally, S., Man, J., Louse, M., Mangum, B., Mapua, P., Martin, K., Martin, R., Mangum, B., Mapua, P., Martin, K., Martin, K., Martin, K., Martin, R., Mangum, B., Mangum, B., Mangum, B., Mandlor, C., Paul, M., Perez, A., Perez, M., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Reick, K., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Reick, K., Reigh, R., Reilly, M., Sanders, A., Soctt, G., Shatsman, S., Sherty, G., Shverr, S., Soctt, G., Shterr, C. D., Shvert, Shrety, J., Shverty, G., Shverr, Sisson, I., Sitter, C.D., Smangs, D.,
117121 TACTAATTTATATAGGGGTATTTAAGGCCCTCTGAGTTAAAGAAACTGTCCTCATCCCGTG 117180
                                                                                                                                   117061 GAGGGGGAGTGAATGGACCCAGTGGGTGTCTTATTTAAAGTGGTTGTGTATGATTCTTA 117120
                                                                                                                                                                                                                                                                                                                                                                             A linear HTG 23-NOV-2002
*** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                          404
                                                                                                                                                                                                                                                                                                                           405 TGTTCA--ATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAACAGTTAAA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomí,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                          286 AGAGGGTAGTGGGTGGGTAGGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTA
                                                                                                                                                                                                                 AC136814.2 GI:25188346
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC136814 208810 bp DN?
Rattus norvegicus clone CH230-179117,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 208810)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117241 AGCTG 117245
                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 AGCTG 467
                                                                                                                                                                                                              346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC136814
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Submitted (23-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
ON Nov 23, 2002 this sequence version replaced gi:24796687.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas sasembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working daraft' sequence. It currently consists of l contiges. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases I to 208810)
Rat Genome Sequencing Consortium.
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Zefeimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C. Taylor, T., Thomas, N., Thomas, A., Tringey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Walliams, G., Wallisana, D., Walczyk, R., Wooden, H., Worley, K., Wight, D., Wright, R., Wu, J., Yen, J., Yoon, J., Yoon, V., Wright, D., Wright, R., Woll, Y., Yoon, V., Wight, D., Weiss, R., Smith, S., Yen, J., Yoon, V., Welnstock, G. and Gibbs, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap, version 0.990329
Consensus quality: 122829 bases at least Q40
Consensus quality: 195654 bases at least Q30
Consensus quality: 197568 bases at least Q20
Estimated insert size: 201423; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: CH230-179117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 208810)
Rat Genome Sequencing Consortium.
Direct Submission
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Gasvant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitling, M., Madan, A., Young, A.C., Shevchenko, Y. Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Samilus, D.E., Schnerth, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 35 Row: 6 Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7304894. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAH20015.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months old, gross tissue."
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (19-DBC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="LocusID:30878"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="apelin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 3143)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .3143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35126 TACTAATTTATATAGAGATATTAAGGCCCTCTGAGTTAAAGAAACTGTCCTCATCCGGTG 35185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35186 TGITCACTATGITTICTAAAAAATGITCCATGTAAATATGITCTTTATAATAAAAAAAAA 35245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34766 TGATTGCCTATTCACCCGTCCCAAAATCCTTCCCATCTGCTGCTGCTAATGCTGCTGCTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34826 CTGCTGCCGCTTCAAGGCCCACCCTGGGGAGCTGGGCCAGTCATAGAGTCCTCACTCCTT 34885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34886 GGGCTTGAAGTGGGGGCTTGCTGGTGCCTCTTCTACTGCTGGTACCCCTGCCAGGGACCA 34945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34946 GGCCTTCTCTGTCTTTGTTGTTTTTGTACCTCTTGCCTTATCAGCCTGCCATGGCCAATC 35005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35066 GAGGGGAGTGAATGGACCCAGTGGCTGTCTTATTTAAAGTGGTTGTATGATTCTTA 35125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (baes 1 to 3143)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROD 12-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 TCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTC----- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 CIGCIGCIGCITAAAGGCICAIGCIIGGAGIGGGGACIGGICGGIGCCCAGAAAGIC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 -----CTTTCTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCCAGCC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405 TGTTCA--ATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAAAACAGTTAAA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC020015 3143 bp mRNA linear ROD 12-NOV-.
Mus musculus apelin, mRNA (cDNA clone MGC:27819 IMAGE:3483588),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 AGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 CCGTGGGGAAGGGGA--GAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 208810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 3.3e-29;
0; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 151.8; DB 2;
Pred. No. 3.3e-29;
                                                                                                                                                                                                                                                                                                                                         /note="wgs_end_extension
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC020015
BC020015.1 GI:18043669
               clone_end:Sp6
                                                                                                                                                                                                                     clone_end:T7_
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.5%;
Similarity 63.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 307; Conservative
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This sequence was finished as follows unless otherwise noted: all
                                                      4;
                                                                                                                                                    2300
                                                                                                                                                                                                                                                  2361 T------TGGCTGAĞAAĞAĞAĞAĞAĞAĞAİAĞA-AĞCACAAĞAĞĞĞĞĞĞĞĞ
                                                                                                                                                                                                                                                                                                                                                                                                                                          2406 GGGCCCAGIGGGCIGICTIAITIAAGIGGITAIGIGIAITICTIAIACTAAITIAIAIA 2465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL714010 118604 bp DNA linear ROD 31-JAN-2003
Mouse DNA sequence from clone RP23-455F14 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
                                                                                                                                                                                                                                                                                                                                                                                                   359
                                                                                                     179
                                                                                                                                                                                                180 GIGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCCAGCCCCGTGGGGAAGG 239
                                                                                                                                                                                                                                                                                                      299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 AAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCC-----TGTGTTCAAT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (31-JAN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2003 this sequence version replaced gi:28172249.
Sequence from the Mouse Genome Sequencing Consortium whole genome
                                                                                                  121 GTCTTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTCCCCCT-TCCTTTCT
                                                                                                                                                 2241 GCCTCTTCTACTGCTGGTACCCTACCAGGACCGGGCCTTCTCCGTCTTTGTCGTTTTCT
                                                                                                                                                                                                                                                                                              240 GGAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGT
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                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 GITTGTAAAGATTGTTCTGTAAATATGTCTTTATAATAAGAGGTG 467
                                                    23;
  DB 10; Length 3143;
                                                    Indels
                                              87;
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27.8%; Score 129.8; DB 69.0%; Pred. No. 2e-23; ive 0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                       Local Similarity 69.0
hes 245; Conservative
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                       Best Loca
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118180 T-------TGGCTGAGAAAGAGGAGATAGA-AGCACAAGAGGGGGGGTAAAAC 118136
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This sequence was finished as follows unless otherwise noted: all
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Submitted (01-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquirles:
Lumquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 2, 2002 this sequence version replaced gi:20330317.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are amnotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission.
numbers given in the feature table with their source databases:
Em:, EMBL; SW:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPE database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-455F14 is
from the RPCI-23 Mouse BAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 GGGCTAGGGGGGCCTGCCTTATTTAAAGTGGTTGTTTATGTTTCTTATACTAATTTTATACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 GTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCAGCCCCGTGGGGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTCTTTCCCCCT - TCCTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                          constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 118604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 129.8; DB 10;
Pred. No. 2.3e-23;
0; Mismatches 87;
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                                                                                                                                                                                                                                                                                                             1. .118604
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP23-455F14"
/clone_lib="RPCI-23"
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Best Local Similarity 69.0%;
Matches 245; Conservative (
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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, GANISSPROT; Tr:, TREMBL; WORNDEPP; Information on the WORNDEPP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1471 GAGATATTAAGGCCCTTTGAGTTAGAGAACTGTCCCCTTCCCATAAGTGTGTTCGCTAT 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1576 T-------TGGCTGAGAAAGAGGAGAGATAGA-AGCACAAGAGGGGGAGTAAAC 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1531 GGGCCCAGTGGGCTGTCTTATTTAAAGTGGTTATGTGTATTTCTTATACTAATTTATATA 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROD 20-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2. (bases 1 to 203805)
Birren,B., Lincon,L., Nusbaum,C., Lander,B., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 GTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAAGCCCAAGCCCCGTGGGGAAGG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCC-----TGTGTTCAAT 412
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 203805)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-15417
                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-351G20 is from the RPCI-23 Mouse PAC Library—constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1696 GCCTCTTCTACTGCTGGTACCCCTACCAGGGACCGGGCCTTCTCCCGTCTTGTCGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 GGAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 GGGCTAGGGGGGCTGCCTTATTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1411 GITIGIAAAATIGITCCATGIAAATATGICTTIATAAAAAGAGTTAAAAAGTIG 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 129.8; DB 10; Length 189982; Pred. No. 2.3e-23; 0; Mismatches 87; Indels 23; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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db_xref="taxon:10090"
/chromosome="X"
/clone="RR23-551G20"
/clone="RR23-551G20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203805 bp
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Best Local Similarity
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Compopismon, Cantellan, Chepellano, K. Changel, M. Collins S., Galdes S., Garden, M. Collins S., Garden Flerent, Carad Flerent

Research

------ Genome Center Center: Whitehead Institute/ MIT Center for Genome

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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
Center_project_name:_L8049
                                                                                                                                                                              /clone="RP23-15417"
/clone lib="RPCI-23 Female Mouse BAC"
1916. _2052
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3233
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14912. 14944
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complement(16705. 16737)
/rpt family="L2"
16753. 16885
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/rpt_family="LIMC5"
complement(4411, .4602)
/rpt_family="MIR"
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/rpt_family="MER2B"
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/rpt_family="B2_Mm2"
                                                                                                                        l. .203805
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complement (7384. .7653)
/rpt_family="LIMB7"
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complement(9871, .9923)
/rpt_family="ID3"
                                                                                                                                                                                                                                                                                                                                                                                                                       complement (6739. .6832) /rpt_family="MIR"
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13818. 13994
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                                                                                                                                                                                                                                                                                                                                                               /rpt_family="(TCC)n"
6408. .6540
                                                                                                                                                                                                                                    2110. .2157
/rpt_family="(A)n"
3485. .3584
/rpt_family="LIMCS"
                                                                          Center clone name: 154 I
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family="(TG)n"
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family="URR1A"
                                                                                                       Location/Qualifiers
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2110. .2157
                                                                                                                                                                                                                                                                                                                                                                                                          family="MIR"
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:complement(13233
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Center code: WIBR
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102060 GGGCCCAGTGGCTGTCTTATTTAAAGTGGTTATGTGTATTTCTTATACTAATTTATATA 102119
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Homo sapiens full length insert cDNA clone ZD38F03.
AF086248 GI:3483593
                                                                                                                                                                                                                                                                                                                                                     /rpt_family="Bl_MM"
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complement(17518. .17565)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="Lx8"
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19919. .2004
                                                                                                                                         'rpt_family="MER31A"
.9703. .19746
                                                                                                                                                                                                                      | (16) n" | (16)
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2364. .22420
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2732. .22777
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|rpt_family="ID5"
|2421. .22448
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
/db_txfe="taxon:32630"
/db_txfe="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01 0.0000.001 TO 0.349.380-seq 02 0.300.001
649.980-seq 01 0.0000.001 349.980-seq 06 1.500.001
1.849.980-seq 05 1.200.001 1.549.980-seq 06 2.000.001
2.449.980-seq 09 2.400.001 2.149.980-seq 10 2.700.001
3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001
3.649.980-seq 13 3.600.001 3.673.778 <223>-Original length
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                    Rattus sp.
Buttus sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalía; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Diagnosis of known genetic parameters within the mhc
Patent: WO 0200932-A 13 03-JAN-2002;
Epigenomics AG (DE)
                                                                                                                                                                  Rosenthal, A., Hinzmann, B., Schaefer, R., Zuber, J., Grips, M., Hellriegel, M., Schmitz, A.C. and Sers, C. Detection of differential gene expression Patent: WO 0157059-A 884 09-AUG-2001; Metagen Gesellschaft fuer Genomforschung mbH (DE) Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 13 from Patent W00200932.
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
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Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted
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                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 598)
Woessner, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J., Marth, G., Bowles, L., Wylie, T., Bowers, Y., Steptoe, M., Theising, B., Geisel, S., Allen, M., Underwood, K., Chappell, J., Person, B., Gibbons, M., Harvey, M., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S., Swaller, T., Behymer, K., Hillier, L., Full Clone Sequencing of the Longest Available Member from Each Unisque Cluster
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/clone="IMAGE:342941"
/clone=lib="Soares_fetal_heart_NbHH19W"
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FLI CDNA.
Homo sapiens (human)
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Waterston, R.
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                                              Homo sapiens
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of seq 2: 3.673778 <2223>-split as follows.~seq 14
0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16
0.000.001 949.980-seq 17 90.001 1.249.980-seq 18 1.200.001
1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001
2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001
3.349.980-seq 23 2.700.001 3.049.980-seq 24 3.000.001
3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             42743 GAGTGGAAGTITGGAAGGGGAGGGTTTGTAATTTATTTGGAAGATTGTGATTGAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 GGTAGTGGGTGGGCTAGGGGGGCTGCTTATTTAAAGTGGTTGTTTATGATTCTTATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42803 ATTGAGGAATGGCGTAAGGAGGAATCGTTTTTTATAGTATTGATTTTATATTATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 AATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCTGTGTTC
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                                                                                                                                                                                                                                                                                         9.9%; Score 46.4; DB 6; Length 73778;
50.0%; Pred. No. 0.31;
ive 0; Mismatches 116; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 AATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAACAGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of known genetic parameters within the mhc Patent: WO 0200933-A 12 03-JAN-2002; Epigenomics AG (DE)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 12 from Patent WO0200932.
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AX344561.1 GI:18492447
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Best Local Similarity 50.0%;
Matches 116; Conservative
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synthetic construct
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Matches 116; Conserv
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VERSION
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AX344561
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342863 TTTTGTTTTAGTTTTAGTTTTAGGGAGAGAGTTAAGGAGAGAAAATGTTTGTTTGGTTTT 342922
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Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Eukaryota; Viridiplantae streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthatroideae; Oryzae; Oryza.

1 (bases 1 to 134971)
Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Gansberger,K., Jones,K.M., Overton II,L., Tsitrin,T., Kim,M., Bera,J., Jin,S., Fadrosh,D.W., Tallon,L., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S., Riedmuller,S.B., Utterbach,T., Feldblyum,T., Yang,Q., Haas,B., Sun,B., Peterson,J., Quackenbush,J., White,O., Salzberg,S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group) chromosome 11 clone
OSJNBa0059H21, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.
230 GTGGGGAAGGGGAGAAAGTGGGGATGGCTAAGAAAAGCTGGGAAGATAGGGAACAGAAGAG
                                                                             342743 GAGTGGAAGTTTGGAAGGGGAGGGTTTGTAATTTATTTGGAAGATTGTGATTGAAAAGG
                                                                                                                                                                                                                                                                                                                                                               350 AATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTC
                                                                                                                                                                                                                                                                         342803 ATTGAGGAATGGCGTAAGGAGGAATCGTTTTTTATAGTATTGATTTTATATTATTTTT
                                                                                                                                                                             GGTAGTGGGTGGGCTAGGGGGGGGCTGCTTATTTAAAGTGGTTGTTTATGATTCTTATACT
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* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 29814 29913: contig of 29813 bp in length
* 29914 53824: contig of 23911 bp in length
* 53825 53924: gap of unknown length
* 53825 53925 71255: contig of 17331 bp in length
* 71256 115072: contig of 43717 bp in length
* 11573 115722: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic Research,
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* NOTE: This is a "working daraft' sequence. It currently a consists of 5 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .134971
/organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 AATGITIGIAAAGATIGIICIGIGIAAAIAIGICITIAIAAIAAACAGITAA
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Submitted (27-MAR-2002) The Institute for Ge
Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 134971)
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1 (Jobes 1. C. 2.1289)

Allen, C. Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, B., Badarin, D., Bandaranaike, D., Barber, M., Baca, E., Baden, H., Baldarin, D., Bandaranaike, D., Barber, M., Barstead, M., Benahmed, F., Bryant, N., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brawlo, K., Carter, K., Cavazos, I., Ceasar, H., Center, A., Carders, V., Carter, K., Carder, M., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, G., Chen, R., Chen, Y., Chen, G., Chen, R., Chen, Y., Chen, G., Davila, M., L., Davis, C., Davyla, M., Cree, A., D'Souza, L., Delgado, O., Danson, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Bapar, A., Escotto, M., Eugene, C., Evans, C.A., Galls, T., Fan, G., Farser, C.M., Gabisi, A., Gancia, R., Garcia, A., Garner, T., Gebregorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Gabisi, A., Gancia, R., Garcia, A., Garner, T., Gabisi, A., Gancia, R., Garcia, A., Garner, M., Hanlandez, S., Haladun, S.L., Hodgson, A., Hernandez, J., Havells, S., Hulyk, S., Huly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28637 WWWYMMMWYSRAWITWWTWRSCSSCYKSCMMWRKYSSYYCYKGKKKYSSCYKKYCSSCSR 28696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC134496 212887 bp DNA linear HTG 20-NOV-2002 Rattus norvegicus clone CH230-402H13, WORKING DRAFT SEQUENCE, 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                     163 TTTCCCCCTTCCTTTCTGTGTCTGCCTGCCTCATCGGCCTGCCATGACCTGCAAGCC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 CAGCCCCGTGGGGAAGGGGAAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAAC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                         Query Match 9.6%; Score 45; DB 2; Length 134971; Best Local Similarity 12.6%; Pred. No. 0.75; Matches 18; Conservative 85; Mismatches 40; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC134496.2 GI:25139155
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                  /note="japonica cultivar-group"
/mol_type="genomic DNA"
cultivar="Nippombare"
db_xref="taxon:3947"
/chromosome="11"
/clone="OSJNBA0059H21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28757 MRRAARRRAARRGGRRRKTW 28779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 AGAAGAGGTAGTGGGTGGGCTA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 212887)
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AC134496/c
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Direct Submission

Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department Submitted (20-NOV-2002) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, Baylor College of Medicine, One Daylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Randers,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sheethy,J., Strong,R., Sung,A., Sorelle,R., Sosa,J., Stelmle,M., Strong,R., Yulton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T. Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Vallas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,G., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Woden,H., Worley,K., Wright,D., Wright,D., Wright,D., Wulu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence It currently

* Consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department
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------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 202261 bases at least Q40
Consensus quality: 204675 bases at least Q30
Consensus quality: 205966 bases at least Q20
Estimated insert size: 205697; wm-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Genome Sequencing Consortium.

Direct Submission

Submitted (27-SEP-2002) Human Genome Sequencing Center, Departmen

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

Rat Genome Sequencing Consortium.
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Center code: BCM
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------ Project Information
Center project name: KBRX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---- Genome Center
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seq29-na-truncated.rge

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REFERENCE
AUTHORS
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JOURNAL
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AUTHORS
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JOURNAL
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
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Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chaveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36597 CTGCTGCTGCTGCTGCTGCTGCTGCTGTTGGTGCAGTGGTGGTGGTCCCTGCTGTT 36538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36657 rgAcAgCrGcrGcrccccrAcrgGrGccrcrGcrrcrGcrrcrGcrGcrGcrGcrGcrGcrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACLUSA82 272030 bp DNA linear HTG 09-NOV-2002
Rattus norvegicus clone CH230-20G17, WORKING DRAFT SEQUENCE, 13
unordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTAACGCTGCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 9.6%; Score 45; DB 2; Length 212887; Local Similarity 58.6%; Pred. No. 0.76; es 78; Conservative 0; Mismatches 55; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACIO5482.4 GI:24818814
HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULITOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                                                                                                    /note="wgg end_extension
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                                                                                                                                                                                      1816. .. 2986
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                                                                                                                                                                                                                                                   clone_end:T7_
site:
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AC105482
LOCUS
DEFINITION
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SOURCE
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Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
Jackson, L., Jacob, L., Jiang, H., Johnson, R., Johnson, R.,
Jackson, L., Jacob, H., Jang, H., Johnson, R., Johnson, R.,
Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
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Lorensuhewa, L., Loulseged, H., Lozado, R.J., Longare, S.,
Mahashwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mayua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., Molecod, M.P., Mowell, T. Z., Menema, E.,
Milosavljevic, A., Miner, G., Munidasa, M., Murphy, M., Nair, L.,
Nandelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pannkoct, C.,
Plopper, P., Pooldexter, A., Poole, M., Rose, M., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Rose, M., Rose, M., Richards, S., Shen, H.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Stefulle, M., Strong, R., Sutch, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, M., Thomas, S., Tingey, A., Tabor, P., Taylor, T.,
Wang, A., Wailson, R., Wilsen, W., Wailson, L., Wailer, R., Wails, W.,
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Winstend, G., and Gibbs, R.A., Smith, D.R., Smith, H.O.,
Winstender, G., Song, R.A., Smith, D.R., Smith, H.O.,
Winstender, G., Share, M., Wales, R., Smith, D.R., Smith, H.O.,
Winstender, G., Share, M., Wales, R., Wales, R.,
Wallay, R., Waless, R., Wales, R.,
Wallay, R., Waless, R., Wales, R., Wales, R.,
Wallay, Wallay, R.,
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On Nov 9, 2002 Linis sequence version replaced gi:23267948.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.lmc.edu/projects/rat/). Each config described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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3 (bases 1 to 272030)

Rat Genome Sequencing Consortium.

Direct Submission
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Consensus quality: 255866 bases at least Q40
Consensus quality: 259606 bases at least Q30
Consensus quality: 269083 bases at least Q20
Estimated insert size: 263005; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center project name: GNAU
Center clone name: CH230-20G17
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Worley, K.C.
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Center project name: L16056
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                                                                                                                                                                  AC101159.1 GI:17059933
HTG; HTGS PHASE0.
Mus musculus (house mouse)
Mus musculus
                              65053 GCTTCTGCTACTG 65065
                                                                                                                                                                                                                                                                                                                                          (bases 1 to 71781)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIBR
   124 TCTTCTGCCACTG 136
                                                                                                                                                  AC101159
                                                                                                                                DEFINITION
                                                                                                                                                                                                                     ORGANISM
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                  RESULT 28
AC101159
                                                                                                                                                    ACCESSION
                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                          REFERENCE
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                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a "working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 CIGCIGCIGCITAAAGGCICAIGCIIGGAGIGGGGACIGGICGGIGCCCAGAAAGIC 123
Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 TGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
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                                                                                                                                                                                                                5173: contig of 5173 bp in length 5273: gap of unknown length 15912: contig of 10539 bp in length 15912: gap of unknown length 15593: contig of 3681 bp in length 19693: gap of unknown length 19693: gap of unknown length 258497: contig of 238804 bp in length 258597: gap of unknown length 258597: gap of unknown length 259907: contig of 1210 bp in length 259907: gap of unknown length 259907: contig of 1210 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                        length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown length
of 1158 bp in length
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bp in length
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gap of unknown length
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contig of 2103 bp
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contig of 1427 b
gap of unknown l
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gap of unknown
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15913. 17329
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237547. 238337
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HTG 23-NOV-2001
                                                                                                                                                                                      Sciurognathi, Muridae; Murinae; Mus.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus Loases, 1 to 71781)

Birren, B., Linton, L., Musbaum, C. and Lander, E.

Mus musculus, clone RP23-173D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
AC101159 71781 bp DNA linear HTG 23
Mus musculus clone RP23-173D8, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads * and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for * identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              737: contig of 737 bp in length
837: agp of 100 bp
555: contig of 718 bp in length
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                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Büteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AC119515.5 GI:25012225
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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KEYWORDS
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The genome Sequencing Consortium.

In the feature of Manage Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23616941.

The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas and whole genome shorgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contigs are consist entirely of whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads.
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* NOTE: This is a "working draft' sequence. It currently NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
* This sequence will be replaced by the finished sequence as soon as it is available and by the finished sequence as soon as it is available and the accession number will be preserved.
* The accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: CR30-40602

Assembly program: Phrap, version 0.990329
Consensus quality: 197852 bases at least Q40
Consensus quality: 197852 bases at least Q30
Consensus quality: 201933 bases at least Q30
Estimated insert size: 207854; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
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'db_xref="taxon:10116"
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206919. .208667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: GUQW
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211434. .213417
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clone_end:Sp6"
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Matches 106; Conservative
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Direct Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On May 13, 2003 this sequence version replaced gi:22855692.

The sequence in this sequence version replaced gi:22855692.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold') Within each contig-scaffold', within each contig-scaffold, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 242655)
Worley,K.C.
Direct Submitted (12-07M-2002) Human Genome Sequencing Center, Department Submitted (12-07M-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 242655)
Rat Genome Sequencing Consortium.
Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wight, D., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhou, X., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Atlas 3.0;
Consensus quality: 230159 bases at least Q40
Consensus quality: 232877 bases at least Q20
Consensus quality: 234876 bases at least Q20
Estimated insert size: 245378; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Baylor College of Medicine Center code: BCM
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Center clone name: CH230-86H10
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/db_xref="taxon:10116"
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2365. .5223
/note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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MAINTY, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyaci, A., Anguiano, D.,
Bandaranaike, D. Barber, M., Baca, E., Baden, H.,
Baldakin, D., Bandaranaike, D., Barrell, K., Calderon, E.,
Cardenas, V., Chavez, D., Chen, E., Ceasar, H., Center, A.,
Carvez, C., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Blair, J., Char, C., Chen, Z., Chen, Z., Chu, J.,
Caveland, C., Corkrell, R., Cox, C., Coyle, M., Cree, D. B'souza, L.,
Davila, M.L., Davis, C., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dedarich, D.,
Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dedarich, D.,
Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dedarich, D.,
Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dedarich, D.,
Davila, M., Becche, M., Elago, M., Porbes, L., Feater, M., Goster, P.,
Feraser, C.M., Gabie, A., Ganta, R., Garcia, A., Garrer, T.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Gherra, M., Guevara, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Gherra, M., Guevara, M.,
Gebregeorgis, E., Geer, K., Gill, R., Johnson, R., Jolivet, A.,
Jackben, L., Jacob, L., Janagh, H., Johnson, R., Johnson, R., Johnson, R.,
Jackson, L., Janagh, H., London, P., London, R., Johnson, R., Johnson, R.,
Jackson, L., Janagh, H., London, P., London, P., Lopez, J., Martin, Y., Martin, K., Martin, R., Marti
                                                                                                                                                                        Partition of the State of States of 
                                                                                                                                                                                                                                                                   352 TITATACAAAGATATTAAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAA 411
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                      292 TAGTGGGTGGGCTAGGGGGCTGCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAA
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSRORI; Tr:, TREMBL; WP: MORNEEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                              191538 TGGTGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAGTAGTTTAGGAATCCACTAGAAA 191479
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Mouse DNA sequence from clone RP23-173D8 on chromosome 4, complete
                                                                                                                                                                                                                                                                                                292 TAGTGGGTGGGCTAGGGGGGCTGCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-OCT-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 3, 2002 this sequence version replaced gi:23337158.
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                                                                                                                                                                                             232 GGGGAAGGGGAGAAAGTGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                352 ITTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTTCAA
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For further details see http://www.chori.org/bacpac/home.htm
                                                                                          Score 44.2; DB 2; Length 242655; Pred. No. 1.2;
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0; Mismatches 103; Indels
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Center code: SC
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Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                       /note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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237046. .239139
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                                                                                             Query Match 9.5%;
Best Local Similarity 50.7%;
Matches 106; Conservative
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misc_feature
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ORGANISM
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AL606973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
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KEYWORDS
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COMMENT

FEATURES

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139975 AATGGAGGGGTTTCACTGTACAAAAGGGCCCAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGC
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Pan troglodytes chromosome UNK clone RP43-16B7, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-AUG-2003) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 173254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequencing Center, 4444
) 63108, USA
                                                                                                                                                                                                                                                                                                                                                   2 AAIGITIGCCIAICCACCTCCCCCAAGCCCCTTTACCTAIGCTGCTGCTAACGCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140035 TGCTGCTGCTGCTGCTAAAGCAGACTAAAGTTGGACTGTGGGATCTTCAGTTCC 140087
                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 TGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGGACTGGTCGGTGCC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-AUG-2003) Genetics, Genome Sequencing Center, Forest Park Parkway, St. Louis, MO 63108, USA On Aug 23, 2003 this sequence version replaced gi:33621016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence..It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                   Length 243369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 164865 bases at least Q40
Consensus quality: 166558 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of Pan troglodytes clone
                                                                                                                                                                                                                                                                  1.2;
                                                                                                                                                                                                                                   Score 44.2; D
Pred. No. 1.2;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: M13; 0%
organism="Mus musculus"
                  /mol_type="genomic DNA"
/db xref="taxon:10090"
/db xref="taxon:10090"
/db xref="taxon:10090"
/db xref="taxon:10090"
/dclone="RP23-173D8"
/clone_lib="RPCI-23"
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC146436.2 GI:34147022
HTG; HTGS PHASE1.
Pan troglodytes (chimpanzee)
Pan troglodytes
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                                                                                                                                                                                                                                Query Match 9.5%;
Best Local Similarity 61.9%;
Matches 70; Conservative
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AF41245 903 bp mRNA linear INV 19-NOV-2001
Nephila clavata dragline silk protein spidroin 2 mRNA, partial cds.
AF441245
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2 (bases 1 to 903)

Ma.H.W., Zhang, L.S. and Zhang, Y.J.

Direct Submission

Submitted (30-00T-2001) Biochemistry Section, Faculty of Basic
Courses, Quartermaster University, 175 Xi'an Road, Changchun, Jilin
                                                                    162 CTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGC 221
                             42 GCTGCTGCTAACGCTGCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277
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                                                                                                               102 ACTGGTCGGTGCCCAGAAAGTCTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTT
                                                                                                                                                                                                                                                                                    222 CCAGCCCCGTGGGGAAGGGGGAGAAGTGGGGATGGCTAAGAAAGCTGGGAATAGGGAA
                                                                                                                                                                                                                                                                                                                                                                        282 CAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAAGTGGGTTGTTTATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 CIGICGGGGICCITGINGICGGGGICCAGICCIGGICCIGCIGCIGCGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'organism="Nephila clavata"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:70342"
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Best Local Similarity 50.2
Matches 108; Conservative
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Nephila clavata
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130062, China
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AF441245/c
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AUTHORS
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KEYWORDS
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  soon as it is available and the accession number will
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                                      contig of 2082 bp in length gap of unknown length contig of 1700 bp in length contig of 1700 bp in length contig of 1260 bp in length gap of unknown length gap of unknown length contig of 1664 bp in length contig of 1463 bp in length gap of unknown length gap of unknown length contig of 17143 bp in length gap of unknown length gap of unknown length
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of 37552 bp in length
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of 73885 bp in length
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165330. 167379
/note="assembly_name:Contig51"
167480. 168940
/note="assembly_name:Contig54"
16941. 170155
/note="assembly_name:Contig72"
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/note="assembly_name:Contig108"
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/note="assembly_name:Contig112"
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/note="assembly_name:Contig115"
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/note="assembly_name:Contig116"
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/note="assembly_name:Contig103"
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/note="assembly_name:Contig110"
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64469. .165829
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/note="assembly_name:Contig99"
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="UNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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170155: 0
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Submitted (17-DEC-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 17, 2003 this sequence version replaced gi:28933642. All repeats were identified using Repeat
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Mammalia; Butheria; Primates; Cararrhini; Hominidae; Homo.
1 (Dases 1 to 119790)
Griffiths, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 155665;
                                                                                                                                                   Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12796: contig of 12796 bp in length 12896: gap of 100 bp 59863: contig of 46967 bp in length 59863: gap of 100 bp 93811: contig of 31848 bp in length 93911: gap of 100 bp 114271: contig of 23360 bp in length 114271: gap of 100 bp 130845: contig of 16474 bp in length 130845: contig of 24720 bp in length 13565: contig of 24720 bp in length
                                                                                                                                                                                                                                                                                              ch 9.4%; Score 43.8; DB 2; Length 1
1 Similarity 76.1%; Pred. No. 1.6;
54; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .155665
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA
/db_xref="taxon:10090"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="1"
/clone="RP24-395P3"
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Homo sapiens
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      Direct Submission
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Best Local Similarity
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HSDJ989D7
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Sirren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barrach, N., Bastien, Y., Bloom, T., Boguslawkiy, L., Boukhalter, B., Camarata, J., Chang, J., Chasno, T., Engerald, Choopel, Y., Collymore, A., Caok, P., Chang, J., Chang, J., Chang, J., Chang, J., Choopel, Y., Collymore, S., Caok, P., Petrogerald, M., Gago, D., Galagan, J., Fareira, P., FitzGerald, M., Gago, D., Galagan, J., Gardyna, S., Gord, S., Landers, T., Levine, N., Hagos, B., Karatas, A., Kells, C., Landers, T., Levine, R., Indoblad, Th., K., Liu, G., Macdonald, P., Major, J., Mathews, C., Kamat, A., Murphy, T., Naylor, J., Newell, P., Norman, C. H., O'Comnor, T., O'Donnell, P., Nicol, R., Norwan, C., Reterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Talamas, J., Volal, R., Vola, R., Wilson, B., Wux., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Submitted (14-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Search, 320 Charles Street, Cambridge, MA 02141, USA

Sirren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Carmarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, P., Corwis, L., Erickson, J., Faro, S., Dadge, S., Dooley, K., Dornis, L., Erickson, J., Faro, S., Graham, L., Grand-Pierre, N., Hagos, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hagos, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hagopian, D., Hagos, B., Hall, J., Hulme, W., Iliev, I., Manschan, C., Macchan, C., Machalaron, K., Liu, X., Lui, A., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Manthews, C., McCarthy, M., Maddrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., O'Romall, P., O'Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Ramasand, J., Ramasandy, U., Raymond, C., Retta, R., Rae, C., Rogov, P., Spencer, B., Stange-Thomann, N., Schaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Schamen, S., Severy, P., Trayers, Wyman, J., Young, G., Zainoun, J., Zembek, L., Zhmmer, A. and Zody, M., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zhmmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC133581 17-DEC-2003 Mus musculus chromosome 1 clone RP24-395P3 map 1, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces.
                     71 TGCTGCTTAAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCCAGAAAGTCTCTTCTG 130
                                                                      276 géchéchecacerceagarderceagarderceagarderceararceagereareare
                                                                                                                                    216 récredrécraterrefrécedérecrrérrefrécederécharaterrefrécres 157
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 1, clone RP24-395P3
                                                                                                                                                                                                                                                         191 CTCATCGGCCTGCCATGACCTGCAGGCCCAG 225
                                                                                                                                                                                                                                                                                                                 156 recrecedecedecidarecaccrecaserecas 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS PHASE1; HTGS FUL
Mus musculus (house mouse)
Mus musculus
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ORGANISM
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AUTHORS
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154263 TTCCAGCTCCCCCCTCCCAACCGCCGCAGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 INGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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17734. .17987

// hote="LinkBl repeat: matches 5782. .6043 of consensus"

18038. .18183

/note="LinkBl repeat: matches 6174. .6316 of consensus"

/note="LinkBr repeat: matches 2409. .2740 of consensus"

/note="LinkBr repeat: matches 1. .354 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .6095 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .6317 of consensus'
                                                                                                                                                                                                                                                                                                                                                        .6165 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                        .5474 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6168 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 2740. .6162 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5892 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6326 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .378 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 221. .385 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2371. .32509
note="LTR16C repeat: matches 81. .221 of consensus"
                                                                                          /note="MLT1J repeat: matches 13. .513 of consensus"
14687. .14768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MLT1J repeat: matches 124. .196 of consensus" 35934. .36427
/note="match: GSS: Em:AQ429711" 35967. .36020
                                                                                                                          .4687. .14768
'note="HAL1 repeat: matches 271. .360 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MER33 repeat: matches 47. .323 of consensus" 1306. .31349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .400 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .239 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MER7A repeat: matches 1. .345 of consensus"
                                                  .249 of consensus"
                                                                                                                                                                                                     repeat: matches 1. .345 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28283. .28491
/hore="LTRIEA repeat: matches 148. .378 of consens
28592. .28729
/hote="MIR_repeat: matches 26. .167 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10385, .30489

note="MIR repeat: matches 40, .153 of consensus"

10759, .31042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .617 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="22 copies 2 mer tt 84% conserved"
1491. 31825
/note="MER77 repeat: matches 38. .400 of
complement (31606. .32269)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .177 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / 24440. .24524
/note="LiMA10 repeat: matches 6095.
252181. .27841
/note="LiMC1 repeat: matches 3550.
complement(27586. .28074)
/note="match: GSS: Em:AQ605230"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24031. .24127
/note="LiMA10 repeat: matches 5993.
24128. .24439
                                                                                                                                                                                                                                                                                              note="match: GSS: Em:AQ012918"
15807. 16507
note="LiMBZ repeat: matches 5469.
                                                                                                                                                                                                                                                                                                                                                                        16561. 17220

Moote="LiMB2 repeat: matches 4871.

17218. 17509

Moote="LiMB8 repeat: matches 5848.

17581. 17733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13729. .24007
note="LIME1 repeat: matches 5598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MER51B repeat: matches 1. 3154. .33323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="MER8 repeat: matches 87.
                                                                                                                                                                                                                                                   'note="match: GSS: Em:AQ772240"
.5375. .15560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 1.
                                             note="MIR repeat: matches 60. 2659. .13160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                omplement(31606. .32269)
note="match: GSS: Em:AQ266996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="match: GSS: Em:AQ700733"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="match: STS: 5731. .35802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18879. .22631
/note="LIMB7 re
23729. .24007
                                                                                                                                                                     15106. .15438
/note="MER2 re
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note="LTR16C
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note="MER5B 1
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                                                                                        Prequestive closure experience version replaced gi:9714378.

On Aug 22, 2000 this sequence version replaced gi:9714378.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations to prove that the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with nonly a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em; EMBL; Sw.; SWISSROT; Tr.; TREMBL; Wp.; WORMEEP; Information on the WORMEEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence to constructed by the Sanger Centre Chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/HGP/Chromosome 20 http://www.sanger.ac.uk/HGP/Ch
                          Submitted (02-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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/note="LiMBB repeat: matches 5834. .5865 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="TIGGER1 repeat: matches 1. .2418 of consensus"
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11843. .12150
/note="AluSx repeat: matches 1. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="dJ989D7.1 (novel transcript)"
/note="continued from bA199014.1 in Em:AL162504
match: cDNAs: Em:AY007089"
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10382. .10435
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/note="L1M4 repeat: matches 4784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="LIM4 repeat: matches -260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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/clone="RP5-989D7"
/clone_lib="RPCI-5"
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/note="match: GSS:
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/gene="dJ989D7.1"
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/note="L1PA16 repeat: matches 3923. .6157 of consensus" 43715. .43783
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                                                                                                                                                                                                      .2484 of consensus"
                                                                                                                                                                                                                                    note="MLT1A1 repeat: matches 4. .365 of consensus"
                                                                                                                                                                     .2745 of consensus"
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                                                                                                                                     .225 of consensus"
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/note="14 copies 4 mer tata 80% conserved"
45244. .45466
              3568. .36019
/note="13 copies 4 mer agat 100% conserved"
36212. 36570
/note="LTR16A repeat: matches 57. .433 of α
38224. .38413
/note="match: GSS: Em:AZ235965"
note="9 copies 6 mer tagata 75% conserved"
                                                                                                                            /note="L2 repeat: matches 2410.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="L2 repeat: matches 2168.
15535. .45726
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6043. .46146
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46738. .46912
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ö Gaps DB 9; Length 119790; ö 53; Indels 9.3%; Score 43.2; D 58.6%; Pred. No. 2.2; iive 0; Mismatches Query Match 9.3 Best Local Similarity 58.6 Matches 75; Conservative

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115477 AAGICTICACAGAAAICCCIATAGAAGATTITITTITTTIGGAAGAACCIGAIGTITG 115536 115537 AGAAGIGATITCCTIACCTCTCTGTGGCTGTACAGCCAGTIGTGTGAGAATATGTG 115596 324 AAGIGGITGITTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCATTA 383 384 AGAAAITGITCCCTICCCCIGIGITCAAIGITIGIAAAGAITGITCIGIGIAAAIAIGIC 443 g g δ

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ACO93112 Homo sapiens BAC clone RP11-621K10 from 2, complete sequence. ACO93112 DEFINITION ACCESSION VERSION RESULT 36 AC093112 KEYWORDS SOURCE LOCUS

PRI 20-MAR-2002

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 59414)
Sulston, J.E. and Waterston, R. AC093112.4 GI:19551206 Homo sapiens (human) sapiens Ношо ORGANISM

REFERENCE AUTHORS

Genome Sequencing Center, Washington dicine, 4444 Forest Park Parkway, St. Louis, Submitted (23-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA Direct Submission Submitted (20-MAR-2002) Department of Genetics, Washington Submitted (20-MAR-2002) Dark Divenue St. Louis, Missouri 63108, On Mar 20, 2002 this sequence version replaced gi:18873939. (Gases 1 to 59414)
Waligorski, J. and Maupin, R.
Unpublished (2001)
3 (bases 1 to 59414) Toward a complete human genome sequence Genome Res. B (11), 1097-1108 (1998) Submitted (09-AUG-2001) Genome University School of Medicine, MO 63108, USA 4 (bases I to 59414) Waterston, R.H. (bases 1 to 59414) Direct Submission Direct Submission Waterston, R.H. Waterston, R. 99063792 9847074 TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS JOURNAL COMMENT

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Center: Washington University Genome Sequencing Center

Center code: WUGSC Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu

Center project name: H_NH0621K10 Summary Statistics

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 00); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by finished as follows unless otherwise restriction digest This sequence was

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McDherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genteics, Inc. (http://www.resgen.com) or Pieter de Jong vBCTOR: pBACG3.6

The clone sequenced to the left is RPI1-157M22, 2000 bp overlap, the clone sequenced to the right is RPI1-266L10, 2000 bp overlap. Actual start of this clone is at base position 79221 of RPI1-157M22; actual end is at base position 33594 of RPI1-266L10.

NEIGHBORING SEQUENCE INFORMATION:

organism="Homo sapiens" Location/Qualifiers .59414

/mol type="genomic DNA

source

FEATURES

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344. .680

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TA) n" TA) n" TA) n" 11" 11" 11" 11" T_rich" 11" ER1_type" to Homo sapiens EST AW204198	/note="similar to Homo sapiens EST AI740522 (NID:9510881) w916407.x1"	QY 400 CCTGTGTTTGTAAGATTGTTTGTGTAAAATTATATAAAAATTATT	ACCI14853/c ACCI14853 ACCI14853 ACCI14853 ACCI14853 ACCI14853 ACCI14853 ACCESSION ACCI14853 ACCI
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Marny, D. Marie., Marker, M. Lee., Abramon, S., Adams, C., Alder, J., Allen, C., Allen, H., Albarhooks, S., Amin, A., Angulano, D. Allen, C., Allen, H., Albarhooks, S., Amin, A., Angulano, D. Allen, C., Allen, H., Albarhooks, S., Amin, A., Angulano, D. Anyalebechi, V., Bandaranaike, D., Barber, M., Baca, E., Baden, H., Bladwin, R., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bladwin, R., David, S., Baden, H., Barder, D., Carter, C., Carter, S., Chan, Y., Chen, Z., Chu, J., Crater, D., Chare, D., Carter, A., Cavaro, D., Chare, C., Coyle, M., Cree, D., D'Govar, L., David, M., Chen, Y., Chen, Z., Charko, J., Chare, C., Coyle, M., Cree, D., D'Govar, L., David, M., Chen, Y., Chin, T., Para, C., Daramo, C., Daramo, C., Ding, Y., Dinh, H., Dinya, R., Chen, Y., Chin, T., Para, C., Daramo, C., Daramo, C., Ding, Y., Dinh, H., Dinya, R., Chen, Y., Chin, T., Para, C., Daramo, C., Daramo, C., Ding, Y., Dinh, H., Dinya, R., Chen, Y., Chin, C., Coyle, M., Cabisi, A., Cante, M., Carter, M., Cabisi, A., Cante, M., Carter, M., Gabrey, M., Harla, P., Harla, P., Hanger, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, M., Harland, M., Hamil, C., Hamilton, C., Hamilton, M., Harla, P., Harland, M., Hawes, M., Hadden, S., Mall, M., Mall, J., Harla, M., Mallan, M., Mallan Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23816565.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs are conding coaffold', Within each contig-scaffold', in dividual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence Department Submitted (12-MAR-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (Dases 1 to 343,188)

Rat Genome Sequencing Consortium. (bases 1 to 343188) (bases 1 to 343188) Submission Unpublished Worley, K.C. Direct

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may extend beyond the ends of the clone and there may be sequence cortiss within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently
consists of 10 contigs. The true order of the pieces
is not known and their order in this sequence record is
stbirary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Phrap; version 0.990329
Consensus quality: 26870 bases at least Q40
Consensus quality: 276498 bases at least Q30
Consensus quality: 270491 bases at least Q20
Estimated insert size: 281218; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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/db_xref="taxon:10116"
/clone="CH230-271E17"
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Rattus norvegicus clone CH230-15A4, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
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179249. .180714
/note="wgs_end_extension
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/note="clone_boundary
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153800. .179198
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1es 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 TCT 124
misc_feature
                                                          misc_feature
                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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KEYWORDS
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Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On Nov 13, 2002 this sequence version replaced gi:22772291.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarmpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Ferannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,B., Pu,L.-I.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Rilly,M., Reilly,M., Rolas,A., Rose,M., Rose,R., Ruiz,S.J.,
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Shedty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Samis,D.,
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Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,B., Tingey,A., Trabor,P., Taylor,C.,
Valas,R., Vera,V., Villasana,D., Waldcon,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
William,G., Willson,R., Wheczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,U.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederinausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 224334)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                data.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 0.990329
Consensus quality: 2.13159 bases at least Q40
Consensus quality: 215868 bases at least Q30
Consensus quality: 215868 bases at least Q20
Estimated insert size: 221167; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_draft_norms: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: CH230-15A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 224334)
Worley, K.C.
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10059: contig of 10059 bp in length

seq29-na-truncated.rge

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M20136.1 GI:201836

T-cell receptor; beta T-cell receptor; receptor.

Mus musculus (house mouse)

SM Mus musculus (house mouse)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 982)

S Lee, N.E. and Davis, M.M.

T cell receptor beta-chain genes in BW5147 and other AKR tumors.

Deletion order of murine V beta gene segments and possible 5'

regulatory regions

L J. Immunol. 140 (5), 1665-1675 (1988)
                                        /codon_start=1
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SEMNWSALELEDSANYVWYZOTLGKELKFLIQHYEKVERDKGFLPSRFSVQQFDDYH
join(13. .91,221. .228)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE DETA-T-cell receptor gene LVD-J-2.5 region, clone BW12. M20136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source text: Mus musculus (strain AKR) thymoma DNA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 ACCTCCCCAAGCCCCTTTACCTATGCTGCTACTAACGCTGCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                   229. .>513
gene="Tcrb"
product="T cell receptor beta-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="T cell receptor beta-chain"
protein id="PAM40398.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 9.1%; Score 42.6; DB 10;
1 Similarity 78.5%; Pred. No. 2.6;
51; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....(401, .479,609, .957)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
            oin(13. .91,221. .514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:10090"
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/tissue type="thymoma"
join(401, .479,609. 95
                                                                                                                                                                                                                                                                                                                                                              221. .514
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/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon start=1
                                                                                                                                                                                                                                                   <13. .90
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                                                                                                                                                                                                                                                                                                           92. .220
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/number=1
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                                                                                                                                                                                                                                                                                          'number=1
                                                                                                                                                                                                                                                                                                                                                                                                                  /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromosome 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 ATAGA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 TTAAA 81
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LOCUS
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VERSION
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AUTHORS
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MEDLINE
           CDS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
(Dasses 1 to 575)
Behlke, M.A., Huppi, K. and Loh, D.Y.
Tandem linkage and unusual RNA splicing of the T-cell receptor beta-chain variable-region genes
87175599
3470773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUSTCBVC1 575 bp DNA linear ROD 29-APR-199
Mouse germline T-cell receptor beta-chain gene, V-5.2 region gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 TGCCIATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8ource text: Mus musculus (strain C57BL/6) liver DNA.
Location/Qualifiers
1. 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.2%; Score 42.8; DB 2; Length 224334; 75.7%; Pred. No. 2.9; cive 0; Mismatches 17; Indels 0;
10159: gap of unknown length
0 220367: contrag of 210208 bp in length
2 226467: gap of unknown length
8 222524: contrag of 2057 bp in length
5 222624: gap of unknown length
5 224334: contrag of 1710 bp in length
Location/Qualifiers
                                                                                                                      1. .224334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end_sequence:BH323033"
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                                                                                                                                                                                                                                                                                                                                                  8963. 10059
/note="wgs contig"
10160. 12825
/note="wgs contig"
complement [207015. ...
                                                                                                                                                                                        clone="CH230-15A4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M15614.1 G1:201273
T-cell receptor; V-region.
1 of 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119333 TGCTGCTGCT 119342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTGCTGCT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 53; Conserv
            10160
220368
220468
222525
222625
 10060
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                                                                                                                         source
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ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
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MUSTCBVC1
LOCUS
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AUTHORS
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COMMENT
FEATURES
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Direct Submission
Submitted (04-ARR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Duringschire, CB10 1SA, UK. E-mail enquiries:
During sequence assembly data is compared from overlapping:
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with This sequence was finished as follows unless otherwise noted: all
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Mouse DNA sequence from clone RP23-407M20 on chromosome 11,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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0; Mismatches
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/gene="zeste"
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1096. .1658
/gene="zeste"
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/gene="zeste"
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/gene="zeste"
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/gene="zeste"
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Best Local Similarity 56.9%;
Matches 78; Conservative
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SEMNMSALELEDSAMYFCASSLGTGGRHPVLMARHSAPRV"
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DNA-binding; chromosomal localization; gene regulation;
transvection; zeste protein.

Drosophila virilis

Drosophila virilis

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Reoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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Chen, J.D., Chan, C.S. and Pirrotta, V.
Conserved DNA binding and self-association domains of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 982;
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gene="zeste"
codon_start=1
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                                                                                                                                                                                       product="T cell receptor beta-chain"
join(401. .479,609. .616)
gene="Tcrb"
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Drosophila virilis zeste gene, complete cds.
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mol_type="genomic DNA"

db_xref="taxon:7244"

map="chromosome X"

germline
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Mol. Cell. Biol. 12 (2), 598-608 (1992)
92123185
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                                                                           |oin(401. .479,609. .616)
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/organism="Mus musculus"
upstream of XbaI site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="putative"
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                                                                                                                                  617. .>955
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                                                                                                                                                                                                                                                                  <401. .479
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'number=1
                                                                                                                                                                                                                                                                                                                                                                                                                        609. .957
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Best Local Similarity 78.5%;
Matches 51; Conservative
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65

Gaps

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seq29-na-truncated.rge

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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-407M20 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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source

FEATURES

1. .145052 /organism="Mus musculus" /mol_type="genomic_DNA" db_xref="taxon:10090" /chromosome="11" /clone="RP23-407M20" 'clone lib="RPCI-23" Location/Qualifiers

. 0 Gaps 9.1%; Score 42.6; DB 10; Length 145052; 78.5%; Pred. No. 3.3; cive 0; Mismatches 14; Indels 0; C Best Local Similarity 78.5 Matches 51; Conservative Query Match

129089 ATACACCACCCCTCTGGCCTAAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

CTGCT 77 73

129029 CTGCT 129025

RESULT 43 AC128156

ACL28156 199221 bp DNA linear HTG 15-NOV-2002 Rattus norvegicus clone CH230-287H17, WORKING DRAFT SEQUENCE. AC128156 AC120156.3 GI:25007826 HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP. Rattus norvegicus (Norway rat) LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

Rattus norvegicus ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE AUTHORS

1 (Dases 1 to 199221)

S Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allan, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.,
Anyalebechi, V., Aoyadi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D. Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., Da Anda, C., Dederich, D.,
Delgado, O., Denson, S., Dermo, C., Dinh, H., Divya, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
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Gebregeorgis, E., Geer, K., Gill, K., Grady, M., Guerra, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J. Jackson, A.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, M., Hoglus, M.,
Harnandez, R., Hines, S., Hladun, S.L., Hodgson, N., Hernandez, J.,
Harnandez, R., Hanes, S., Hladun, S.L., Hodgson, Hollins, B., Howells, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jang, H., S., Khan, Z., King, L., Kovar, C.,

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

now 15, 2002 this sequence version replaced gi:23906235.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgum sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each config described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold', individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consists entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature Liu,J., Liu,W., Liu,Y., Lebow,H., Levan,L., Lewls, L., Lunda,J.,
Liu,J., Liu,W., Liu,Y., Longaged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwai,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwai,M., Mahtin,K., Martin,R., Martinez,B.,
Mangum,B., Mapua,P., Martin,K., Martinez,B.,
Mangum,B., Mapua,P., Martin,K., Martinez,B.,
Mardiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Murphy,M., Nair,L.,
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Marley Morley, K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 199221)
Rat Genome Sequencing Consortium. Li, Z., Liu, J., Lewis, L., Levan, J., TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL AUTHORS REFERENCE JOURNAL

COMMENT

Center: Baylor College of Medicine ----- Genome Center Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Center clone name: CH230-287H17 GZ00 Center project name:

Assembly program: Phrap, version 0.990329
Consensus quality: 186979 bases at least Q40
Consensus quality: 189196 bases at least Q30
Consensus quality: 190602 bases at least Q20
Estimated insert size: 190707; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently

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Submitted (20-JUL-1997) Department of Molecular Biotechnology, Box Submitted (20-JUL-1997) Department of Molecular Biotechnology, Box 35730 University of Mashington, Seattle, Washington 98195, USA Sequencing methodology, high redundancy shofgun. Based on overlapping cosmids, the precision of this sequence is 99.93. Libraries were derived from two strains but there was no discernable sequence variation between them. This sequence contains numerous internal duplications, especially in the rypsinogen genes. Interspersed Repeats were identified with RepeatMasker (available from http://ftp.genome.washington.edu/RW/RepeatMasker.html) Several new fully classified. Simple sequence repeats were identified with sputhik (available from http://serac.mbt.washington.edu/~chrisa/software/sputnik.html)

The authors thank Christopher Nelson for his gift of cosmids from Dennis Loh's library.
                                    11160223
2 (bases 1 to 250611)
2 (bases L., Koop,B.F., Boysen,C., Wang,K., Ahearn,M.E., Qin,S.,
Lee,I., Seto,J., Acharya,C., Ankener M., Alving,W., Chen,L.,
Paeper,B., Baskin,D., Jerome,N., Swartzell,S., Gilbert,T.,
Faust,J., Loretz,C., Bumgarner,R. and Hood,L.
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Rowen,L., Smit,A.F.A. and Hood,L.
Comparison of the human and mouse T cell receptor beta and
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96883. 131111
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AE000663 AE000522
AE000663.1 GI:2358069
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Chen, F., Rowen, L., Hood, L. and Rothenberg, E.V.
Differential transcriptional regulation of individual TCR V beta segments before gene rearrangement
J. Immunol. 166 (3), 1771-1780 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 TGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTG
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consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 199221: contig of 199221 bp in length.
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MMAE000663
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SOURCE
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McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (Bases 1 to 261600)
Wilson, R. K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 ACCICCCCAAGCCCCTTTTACCTATGCTGCTAACGCTGCTGCTGCTGCTGCTGC
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Mus musculus chromosome 6 clone RP23-45H9, complete sequence.
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Best Local Similarity 78.5
Matches 51, Conservative
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/db xref="taxon"
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/clone="lb="kai wang"
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/note="this gene is similar to human
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/clone_lib="Kai Wang"
horte="Khis cosmid is chimeric.
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/db_xref="taxon:10090"
/dlone="cosmid 47.2"
/clone="cosmid 47.2"
/clone="lib="Kai Wang"
235693 ...>250611
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/rpt family="RMER10A"
13212. .13327
/rpt_family="MYS1_PL"
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/mol_type="genomic DNA"
/strain="BALB/c"
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/mol type="genomic DNA"
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"mol_type="genomic DNA"
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                                                                                                                            'mol_type="genomic DNA"
'strain="BALB/c"
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190216 .220895
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family="URR1A"
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|clone="cosmid 83.1"
|clone lib="Kai Wang"
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/rpt_family="Lx9"
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146. .3201
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rpt_unit="ATATA"
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3 (bases 1 to 261600)
MCPherson, J. D. and Waterston, R.H.
Direct Submission
Submitted (10-MAY-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
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                                                                                                                                       Submitted (12-DEC-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Dec 12, 2003 this sequence version replaced gi:30522940.
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MCPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (22-OCT-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 139786)
Yoakum,M., Kozlowicz,A., Mangiapanello,L., Dignan,G., Haglund,K.
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1 Similarity 78.5%; Pred. No. 3.3;
51; Conservative 0; Mismatches
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/organism="Mus musculus"
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3 (bases 1 to 139786)
MCPherson, J. D. and Waterston, R.H.
Direct Submission
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/chromosome="6"
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Wilson, R.
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                                                                                                   Wilson, R.K.
Direct Submission
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Direct Submission
Submitted (13-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 10, 2003 this sequence version replaced gi:24211432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
5 (bases 1 to 139786)
McMeharson, D. and Waterston, R.H.
Direct Submission
Submitted (10-JAN-2003) Genome Sequencing Center, 4444 Forest Park
Expray, St. Louis, MO 63108, USA
6 (bases 1 to 139786)
Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted:
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Center code: WUGSC
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Location/Qualifiers
1. 139786
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
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/rpt_family="L1"
1231. .120*
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/rpt_family="L1"
2273. .2774
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7500. .7532
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7533. .7724
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12712 GCTGCTGCTGCTGCTGCTGCTGCTGCTGATTCATGTTCATGTTTCATATTTTGTTAGTGG 12653
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Homo sapiens chromosome 5 clone RP11-90P14, WORKING DRAFT SEQUENCE,
6 unordered pieces.
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DOE Joint Genome Institute.

DOE Joint Genome Institute.

District Submitseion

Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Aug 25, 2001 this sequence version replaced gi:14333928.

-----Genome Center
Center: Joint Genome Institute
Center: Joint Genome Institute
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1. (Dases 1 to 155276)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 GCTGCTGCTAACGCTGCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cch 9.1%; Score 42.4; DB 10; Length 139786; al Similarity 72.4%; Pred. No. 3.7; 55; Conservative 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC091992
AC091992. AC1:15290436
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
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Consensus quality: 151184 bases at least Q40
Consensus quality: 153297 bases at least Q30
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/rpt_family="ERVK"
53349 . .53400
/rpt_family="B4"
53406 . .53982
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Center Project Name: 441299
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.2587. .52789
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10974. .51573
rpt family="L1"
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                    7539. .7611
/product="RRA-Ser"
/note="likely pseudogene (HMM Sc=42.00 / Sec struct
Sc=-16.48)"
                                                                                                                                                                                                                                                                                                                                                                                                                      rpt family="RMER19B"
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2175. 21281
21446. 21629
/ Type family="L1"
21446. 21629
/ Type family="L1"
21842. 22285
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38949. 39172
/ Type family="ERVL"
38949. 39172
/ Type family="ERVL"
38949. 39172
/ Type family="ERVL"
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/ Trp. family="L1"
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/ Trp. family="ERVK"
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/ Trp. family="ERVK"
/ Trp. family="L1"
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/ Trp. family="L1"
43379 . 43576
/ Trp. family="L1"
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/rpt_family="MalR"
20714. 20814
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12828. 13019
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7930...8178

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8908...8000

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/rpt_family="L2"
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11307. .11488
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1050. .11303
/rpt_family="B2"
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Wilson, R
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Consensus quality: 153815 bases at least Q20
Estimated insert size: 159750; agarose-fp estimation
Cuality coverage: 15476; sum-of-contigs estimation
Quality coverage: 5.9 in Q20 bases; agarose-fp estimation
Quality coverage: 6.07 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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202733 bp DNA innear ROD 08-NOV-2003 Mus musculus BAC clone RP23-296023 from 3, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 GCAGCCAAGCCCAGCCCCGTGGGGAAAGGGGAAAAGTGGGGAATGGCTAAGAAAGCTGGG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 AGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGGCCTGCTTATTTAAAGTGGTT 331
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

(Dases 1 to 202733)

Abbott,S., Haglund,K., Creason,K. and Schatzkamer,K.

The sequence of Mus musculus BAC clone RP23-296023

Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%; Score 42.4; DB 2; Length 155276; llarity 58.9%; Pred. No. 3.7; Conservative 0; Mismatches 51; Indels 0;
                                                                                                                                                                                                                                        7359: contig of 7359 bp in length 7459: gap of unknown length 17306: contig of 9847 bp in length 17406: gap of unknown length 37466: contig of 20060 bp in length 3756: gap of unknown length 57351: contig of 19785 bp in length 57451: gap of unknown length 91524: gap of unknown length 91624: gap of unknown length 155276: contig of 63652 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .155276
/ Organism="Homo sapiens"
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/ Mb_xref="taxon:9606"
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/ clone=lib="RPCI human BAC library 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing of Mus musculus Unpublished (2001) 3 (bases 1 to 202733) McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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AC122805.4 GI:28195579
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91624:
155276:
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37566:
57351:
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37567
57352
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91525
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7460
17307
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AC122805/c
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Direct Submission
Submitted (08-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 2, 2003 this sequence version replaced gi:24943041.
                        Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 202733)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (13-NOV-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 202733)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (02-FRB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 202733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this schone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
Submitted (25-MAY-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/61 mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
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This sequence is the entire insert of the clone. This clone is
overlapped by AC124343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center
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Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: M_BA0296023
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/rpt_family="L1"
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/rpt_family="L1"
3641. .3745
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3123. .3430
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family="Alu" 4602 4602 8783 8783 family="B4" c. 1602 family="B4" c. 2078 family="L" c. 2512" family="RWER c. 2548 family="RWER c. 2548 family="RWER canily="RWER	Eamily, Eamily	135612 family="171" 136708 family="172" 136708 family="172" 138809 138809 138809 138809 138809 family="Ma 140302 family="Ma 140302 family="171" 141384 family="171" 141386 family="171" family="	amily= .4848 amily=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 GCTGCTGCTAACGCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGG
Parkway, St. Louis, MO 63108, USA
On Oct 12, 2002 this sequence version replaced gi:22475561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
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9.1%; Score 42.4; DB 2; Length 203124;
Best Local Similarity 72.4%; Pred. No. 3.7;
Matches 55; Conservative 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                  Sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 200807 bases at least Q40 Consensus quality: 201808 bases at least Q20 Consensus quality: 201988 bases at least Q20 Insert size: 226000; agarose-fp Insert size: 23987; sum-of-contigs Quality coverage: 12.19 in Q20 bases; sum-of-contigs Quality coverage: 12.19 in Q20 bases; sum-of-contigs
                                                                                   Center: Washington University Genome Sequencing Center
Center code: WUGSC
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10802: gap of unknown length
29554: contig of 18752 bp in length
29654: gap of unknown length
92108: contig of 62454 bp in length
92208: gap of unknown length
203124: contig of 110916 bp in length.
                                                                                                                                  Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
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    .203124
    /organism="Mus musculus"

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/db_xref="taxon:10090"
/chromosome="UNK"
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Baylor Plaza, Houston, TX 77030, USA.
On Nov 19, 2002 this sequence version replaced gi:23322236.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgum sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold') within each contig-scaffold') within each contig-scaffold' by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Phrap; version 0.990329
Consensus quality: 206076 bases at least Q40
Consensus quality: 212212 bases at least Q30
Consensus quality: 212212 bases at least Q20
Bstimated insert size: 201535; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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of 4832 bp in length
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230156: contig of 1095 bp in length
230256: gap of unknown length
231359: contig of 1103 bp in length
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: ngoject Information
Center project name: GWTQ
Center clone name: CH230-436119
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234228: contig of 1324 bp
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    /organism="Rattus norvegicus"

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/note="wgs_contig"

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C 5 454 97.2 668 C 6 447 95.7 450 C 7 440.4 94.3 687 C 8 427.4 91.5 889	9 422.8 90.5 10 420.2 90.0 11 419.2 89.8	12 417.4 89.4 13 416 89.1 14 406.2 87.0	394.6 84.5 391.2 83.8 389.6 83.8	19 384.6 82.4 20 380.6 81.5 21 379.4 81.2	22 338 72.4 23 303.6 65.0	25 269 57.6 26 261 8 56 1	250.8 53.7	29 220.8 47.3 30 200.8 43.0 31 175.6 37.6	148.2 31.7 142.6 30.5	130 ·27.8 129.8 27.8	129.8 27.8 129.8 27.8	129.8 27.8 129.4 27.7	128.8 27.6 127.2 27.2	127 27.2	126.6 27.1	118 25.3	117.8 25.2	107.2 23.0	106.8 22.9 103.4 22.1	102 21.8 95 20.3	92 19.7	88 18 8	87.6 18.8 86 18.4	85 18.2 84.8 18.2	62 82.6 17.7	77.4 16.6	65 76 16.3 66 73.8 15.8	67 73.8 15.8	59 12.6	71 58.2 12.5	72 55.6 11.9 73 54.2 11.6	52.2 11.2 49.6 10.6 48.8 10.4 47.2 10.1	
5.1.6 Compugen Ltd.		ime 2857 Seconds ut alignments) 17 Million cell updates/sec	.taataaacagttaaaagctg 467		ត	: 55026578																					<pre>d by chance to have a the result being printed,</pre>	re distribution.			Description	BM975075 UT-CR-EC1 BEB55577 7910e01.x AI871469 w167409.x CA444588 UI-H-DI1-	
GenCore version 5.1 Copyright (c) 1993 - 2004 Comp	- nucleic search, using sw mode	May 25, 2004, 15:09:31 ; Search time (without a 4881.217 M	SEQ29-NA-TRUNCATED score: 467 :: 1 caatgtttgcctatccacct	able: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	27513289 seqs, 14931090276 residue	oer of hits satisfying chosen parameters	<pre>s seq length: 0 s seq length: 2000000000</pre>	Post-processing: Minimum Match 0% Maximum Match 100%	first	EST:* 1: em			6: em_estpl:* 7: em_estro:*			 8 8 6	13: 90 e854: 14: 90 e855:	ฮู่ ฮู่ ซ ๋ ฮ์	em_gss_hum:	e e e	E E	6 Ha	em gss pro:	em gss prg:	 6		Fred. No. 18 the number of results predicted by score greater than or equal to the score of the	derived by analysis of the	SUMMARIES	Query	Match Length DB	466 99.8 728 12 BM975075 462.2 99.0 555 10 BE855577 456 97.6 482 9 AI871469 454 97.2 517 14 CA444588	
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ALS70843 ALS70843
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/dew_gtage="Adult and Fetal"
/lab.host="DH108 (Life Technologies) (Tl phage resistant)"
/clone lib="UT-CF-EC1"
/clone lib="UT-CF-EC1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not I;
UT-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:191-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, dispested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the NATALLY CONTAINED ANALY CONTAINED AND A CONTAINED AND A CONTAINED AND A CONTAINED ANALY CONTAINED AND A CONTAINED AND A CONTAINED AND A CONTAINED ANALY CONTAINED AND A CONTAINED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-180.
TAG_LIB=UT-CF-EC1
TAG_ESEQ=AAGTGCTTAC"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424 CTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGGACTGGTCGGTGCCCAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 GICICITICIDE COCCOCCATCAGGGATIGGGCCTICITICCCCCTICCTITCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TGTCTCCTGCCTCATCGGCCTGCCATGACCTGCCAAGCCCCAGCCCCCGTGGGGAAGGG
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ALI06008 Drosophil
AM48179 64383 MAR
ALI03735 Drosophil
BX374796 BX344796
BX086456 BX086456
BX381320 BX381320
ALO64073 Drosophil
ALO5966 Drosophil
ALO5966 Drosophil
ALS2019 Tetraodon
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ALS2019 Tetraodon
ALS13975 ALS13975
BH396372 AG-ND-159
BX45732 BRST4875
CD55850 BRST675
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ALO9451 Drosophil
BX34217 BNOWTSTR
CD65987 BRST6737
ALO99451 Drosophil
BX34917 BX34917
CD660017 ERSTGF38
BX360796 BX360796
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UI-CF-EC1 Homo sapiens cDNA clone
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Dr. M. Bento Soares, University of Iowa
Tr. M. Bento Soares, University of Iowa
Bento Soares, University of Iowa
chers may obtain clones from Research
r from Open Biosystems
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s; Catarrhini; Hominidae; Homo.
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Simple_repeat 685-728,
thed compliment)
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/clone=="UI-CF-ECI-acf-l-23-0-UI"
/tissue_type="Lung"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soares, M.B.
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AI871469
482 bp mRNA linear EST 07-MAR-2000 w167d09.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2429969 3' similar to contains element TAR1 repetitive element ;, mRNA
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DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1400P from Gibco
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/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 402) NCI/NTNDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI/NTNDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Josozders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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48 AGATICITICIGIGIAAAIAIGICTITIAAAAAAAAAGCIG
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99.8%; Pred. No. 1.3e-108;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 450.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                AI871469
AI871469.1 GI:5545518
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
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library is AACTGTTCG TAG_TISSUB-lung meta TAG_LIB=UI-H-DT1	TAG_SEQ=AACTGTTCGG" ORIGIN	Query Match 97.2%; Score 4 Best Local Similarity 99.4%; Pred. N Matches 467; Conservative 0; Mism	Oy 1 CAAIGITIGCCTAICCACTCCCCCAA	2y SB CTGCTGCTGCTGCTGCTGCTTAAAAGC		Db 3.68 AAAGTCTTCTTCTACACTGACGCCCCCC Qy 1.78 CTGTGTCTCCTGCCTAATGGCCTGCCT	Db 308 CIGTGTCTCCTGCCTCATCGCCTGCC Qy 238 GGGGAGAAAGTGGGGATGGCTAAGAA		Qy 298 GTGGGCTAGGGGGGCTGCTTATTTAA		128	DD 68 TAAAGATTGTTGTGTAAATATGTGT	RESULT 5	EQUOSIS/C LOCUS DEFINITION UI-H-EIL-aza-n-02-0-UI.sl NCI IMAGE:5846209 3', mRNA sequen	Z	KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens	Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; REFERENCE 1 (bases 1 to 668)		JOURNAL Unpublished (1997) COMMENT Contact: Robert Strausberg, Pl Email: cgapbs-r@mail.nih.gov	Tissue Procurement: Dr. Jose N CDNA Library preparation: Dr. CDNA Library Arrayed by: Dr.	DNA Sequencing by: Dr. M. Ber Clone Distribution: Clone dis through the I.M.A.G.E. Consort	The following repetitive elem sequence: 409-448, > (CAG)n#Sin Seq primer: M13 FORWARD	POLYA-Yes. FEATURES Location/Qualifiers
181 IGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCAGCC	241 GAG-AAAGTGGGGGTGGCTAAGAAACTGGGAAATAGGGAACAGAAGGGTAGTGGGT 299		168 GGGCTAGGGGGGCCTGTTTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACA 109 360 AAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCTGTGTTCAATGTTTGTA 419	108 AAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTGTA 49 420 AAGATTGTTCTGTGTAAAATATGTCTTTTTAABABABABAGTTAGTTTAABABAGTTGTAATGTT	AAGATTGTTCTGTGTAAATATGTCTTTATAATAAACAGTTAAAAGCTG		OLTH-DILAWI-M-08-0-01.SI NOI CGAP DI Homo sapiens CDNA Clone UI-H-DII awi-m 06-0-01 3', mRNA sequence.	CA444BBB.1 G1:48U9008 EST. Homo sapiens (human)	Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 517)	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	Juliol Gene Imaex Unpublished (1997) Contact: Robert Stransberg Db D	Email: cgapbe.remail.nih.gov Tissue Procuremnt: Dr. Jose Mercuende	CDNA LIDIATY PREPARATION: Dr. M. Bento SOARES, University of lowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution.	from Dr. M. Bento Soares, bento-soares@ulowa.edu The following repetitive elements were found in this cDNA sequence: 409-448, > (CAG)n#Simple_repeat	Seq primer: M13 FORWARD POLYA=Yes.		/mol_type="mRNA" /db_xref="taxon:9606" /clos="Ul-H-awl-m-06-0-Ul" /tiense:"Mol="Mol-set="ta"	/ dev stage="Mault" // lab_host="DH10B" (Life Technologies)"	/clone_lib="NCI_CGAP_DTI" /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;	ALL USE THI IS A NOTMALIZED CONA LIDRARY CONTAINING THE FOLLOWING TISSUE(8): Metatastic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon	and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated	to an Ecox 1 adaptor, digested with Not 1, and cloned directionally into pTyT3-per covector. The oligonucleotide used to prime the synthesis of first-errand cDNA contains	a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
oy.			g &	g &		RESULT 4 CA444588/c LOCUS	ACCESSION	VERSION KEYWORDS SOURCE	ORGANISM	AUTHORS TITLE	JOURNAL		·			realores source							

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trausberg, Ph.D.

ail.nih.gov

te. Dr. Jose Mercuende

paration. Dr. M. Bento Soares, University of Iowa

"gyed by: Dr. M. Bento Soares, University of Iowa

"y: Dr. M. Bento Soares, University of Iowa

y: Dr. M. Bento Soares, University of Iowa

on: Clone distribution information can be found

on: Clone distribution information can be found

of. E. Consortium/LINL at: http://image.llnl.gov

ppetitive elements were found in this cDNA

ORWARD
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-UI.sl NCI_CGAP_EII Homo sapiens cDNA clone
NA sequence.
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Primates, Catarrhini, Hominidae, Homo.
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itute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                               Length 517;
AACTGTTCGG.
=lung metatastic chondrosarcoma
-H-DT1
                                                                                                                                                                         0; Indels
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; Pred. No. 4.5e-108;
0; Mismatches 0;
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//done lib="NOT_CAPE EI |

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                                                                                                                /clone="IMAGE:5846209"
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/dev_stage="Adult"
/lab_host="DH10B (Life_Technologies)"
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Pred. No. 4.9e-108;
0; Mismatches 0;
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TAG_LIB=UI-H-EI1
TAG_SEQ=ACACTTGCAC"
                                organism="Homo sapiens"
                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
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467; Conservative
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AI149981 450 bp mRNA linear EST 10-NOV-1998 qf38hl0.xl Soares testis NHT Homo sapiens cDNA clone IMAGE:1752355 3' similar to contains element PTR5 repetitive element ;, mRNA

AIÍ49981 AI149981.1 GI:3678450

ACCESSION VERSION

sequence.

LOCUS DEFINITION

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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image.html
Insert Length: 718 Std Error: 0.00
Seq primer: 40ml3 Wd. ET from Amersham
High quality sequence stop: 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clome_lib="Soares_testis_NHT"
hote="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITAAGAAATIGITCCCTTCCCCTGTGTTCAATGTTTGTAAAGAITGTTCTGTGTAAATAT 440
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 450)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 CCCCATCAGGGATTGGGCCTTCTTTCCCCTTTCTGTGTCTCTGTGCCTCATCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 CCCCCAAGCCCCTTTACCTATGCTGCTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTTTAA
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                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
EmNa Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
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Pred. No. 2.9e-106;
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al Similarity 100.0%; Pred. No. 2.9

447; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:1752355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab host="DH10B"
EST.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                               Tumor Gene Index
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Best Local Similarity
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CIGCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGAACTGGTCGGTGCCCAG 117
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE009YJ24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX434223.1 GI:30777248
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
                                                                                                                                                                                                          CA438256 687 bp mRNA linear BST 08-NOV-2002 UI-H-DTI-avw-g-05-0-UI.S1 NCI CGAP DT1 Homo sapiens cDNA clone UI-H-DT1-avw-g-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dry primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pY773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dY)18 tail. The sequence tag for this
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I (basea I to 687)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="NCT_CGAP_DT1"
/note="Organ: Lung; Vector: pT713-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: NOT I; NCI CGAP_DT1 is a normalized CDNA library containing the following tissue(s): Metatastic Chondrosarcoma in Lung.
                         90 TTAAGAAATTGTTCCCTTCCCCTGTTTCAATGTTTGTAAAGATTGTTCTGTGTAAATAT 31
1 CAATGITIGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTAAAC---GCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from Dr. M. Bento Soares, bento-soaresculova.edu
The following repetitive elements were found in this cDNA
sequence: 409-448, > (CAG)n#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG TISSUE=lung metatastic chondrosarcoma
TAG_LIB=U1-H-DT1
TAG_SEQ=AACTGTTCGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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'tissue_type="Metastatic Chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 94.3%; Score 440.4; DB 14. al Similarity 98.9%; Pred. No. 1.8e-104; 465; Conservative 0; Mismatches 1;
                                                               441 GTCTTTATAAAACAGTTAAAAGCTG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                         30 GTCTTTATAATAACAGTTAAAAGCTG 4
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                        CA438256.1 GI:24802676
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                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                        sapiens
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Matches 465; Conserv
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CA438256/c
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/tissue type="PACENTA" //tissue type="PACENTA" /clone lib="Homo sapiens PLACENTA" /clone lib="Homo sapiens PLACENTA" //note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX434223 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YJ243-PRIME, mRNA sequence.
      369
                                                                                                             368 AAAGTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCTTT 309
                                                                                                                                                                                                                                                                                                                                                       189
                                                                                                                                                                             237
                                                                                                                                                                                                                                       249
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                                                                                                                                                                                                                                                                                                                                                                                                                                            188 GIGGGCTAGGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
428 criccriccriccriccriccriadadecricariccrisdadrodogacriccriccada
                                                                                                                                                                                                        CTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCCAGCCCCGTGGGGAA
                                                                                                                                                                                                                                                                                          GGGGAGAAAGTGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGG
                                                                                                                                                                                                                                                                                                                                     248 GGGGAGAAAGTTGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAACAGAAGGAGGTAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                           GIGGGCIAGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATA
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http://fulllength.invitrogen.com/ lnvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAK025CH09NM1.
_Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAAGATTGTTCTGTAAATATGTCTTTATAATAAACAGTTAAAAGCTG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 TAAAGATTGTTCTGTGTAAATATGTCTTTATAAAAGAGCTTAAAAGCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 889)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Gaps 0; 101

161 318 258 281 198 341 138

401 78

18

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normalized libraries (melanocyte 2NbHW, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools of 340488-345479, and 484488-489479."
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zk85f07.rl Soares pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:489637 5' similar to contains element PTR5 repetitive element
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Bukaryota, Metzaca, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metzaca, Chordata, Catarrhini; Hominidae, Homo.

(Dases 1 to 431)

Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.

and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGCTGCTAACGCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGG 378
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2: Eco RI; Equal amounts of plasmid DNA from three
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                                                                                                                                                                                                                                                                                                                               Length 437;
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                                                                                                                                                                                                                                                                                                                         90.5%; Score 422.8; DB 9;
99.5%; Pred. No. 6.4e-100;
iive 0; Mismatches 2;
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AUTHORS
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                                                                  2
                                                                                                                                                                                 CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTACCTAACGCTGCTG 403
                                                                                                                                                                                                                                                CTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAA 120
                                                                                                                                                                                                                                                                                                   CIGCIGCIGCIGCITATAAAGCICAIGCIIGGAGIGGGGACIGGIGGGGGGGCCCAGAAA 343
                                                                                                                                                                                                                                                                                                                                                                        GICICITCIBCCACIGACGCCCCCAICAGGGAIIGGGCCTICITICCCCCTICCTITCIG 180
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 AGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:2114172"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Scares NhHMPu S1"
/note="Organ: mixed (see below); Vector: pT/T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 551 Std Exror: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
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                                                                                                                              CAATGITITGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTG
                                                                     Gaps
                                                                     4
         889;
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         Length
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         13;
                                     .1e-101;
         DB
   ; Score 427.4; I
; Pred. No. 5.1e-
0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
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      sch 91.5%;
al Similarity 97.8%;
455; Conservative
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Unpublished (1997)
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Best Local S:
Matches 455
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ORGANISM
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pTyT3 vector. Library went through one round of normalization. Library
                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases I to 48)
Hillier,L. Lemon,G. Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hulkman,M., Kucaba,T., Lacy,M., Le,W., Le,N., Ch., Rohlis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Travaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R., Manda, Marchan, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clome lib="Soares pregnant_uterus NbHPU" //note="Organ: uterus; Vector: pT/T3-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dI) primer [5'
                                                                                                                                                                                                                                                                                                               Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 528 Std Error: 0.00 Seg primer: -40Ml3 fwd. from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCATCAGGGATTGGGCCTTCTTTCTCTCTGTGTCTCNCTCTTCGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.8%; Score 419.2; DB 9; Length 458; 97.3%; Pred. No. 5.7e-99; ive 0; Mismatches 11; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Tatta Fark Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
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constructed by M. Fatima Bonaldo."
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xxef="dDB:3804224"
/db_xxef="taxon:9606"
/clone="IMAGE:489637"
IMAGE:489637 3', mRNA sequence.
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                 AA101878.1 GI:1645281
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                                                                          Homo sapiens (human)
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          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@mage.llnl.gov) for further information.
Insert Length: 528 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Soares pregnant uterus NbHPU"
/note="Organ: uterus; Vector: pT/T3-Pac; Site_1: Not I
Site_2: Eco RI; 1st strand cDNA was primed with a Not
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                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="GDB:3804224"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                          clone="IMAGE:489637"
                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="DH108"
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  Contact: Wilson RK
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Matches 422; Conservative
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/clone="Inhace:27libs" /
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/clone="Delib (Life Technologies)" /
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/clone="Delib (Life Technologies)" /
/clone="Vector: pT7130-Pac (Pharmacia) with a modified /
/note="Vector: pT7130-Pac (Library last vector) /
/note="Vector: pT7130-Pac (Library last vec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligomuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 10-SEP-1999
                                                                                                                                                                                                                         TTAAGAAATTGTTCCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATAT 440
TTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCA 380
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1 (bases 1 to 449)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW015212
UI-H-BIOD-aba-e-12-0-UI.81 NCT_CGAP_Sub2 Homo sapiens CDNA clone
IMAGE:2711158 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .449
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Seq primer: M13 Forward
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FEATURES

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1492104-1493255) NCI CGAP LUS pool 1 LLAM 3575-3582, 3851-3854 [IMAGE CloneIDs 141420-1417991, 1520904-152239] NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-375 [IMAGE CloneIDs 1257096-1258831, 1465064-1470983, 1475592-1476743) NCI CGAP F722 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 [IMAGE CloneIDs 985608-986759, 110192-1101359, 1217928-1220615) NCI CGAP F722 pool 1 LLAM 244-2653, 2871-2872 [IMAGE CloneIDs 985608-986759, 110192-1101359, 1217928-1220615) NCI CGAP Colo pool 1 LLAM 2644-2653, 2871-2872 [IMAGE CloneIDs 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 4 million recombinants. Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches TO Facilitate Gene Discovery.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 428)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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TAG_LIB=NCI_CGAP_Brn23
TAG_SEQ=ATATC"
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Homo sapiens
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clone CS0DI012YI10 3-PRIME, mRNA sequence.
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/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site=1: Not 1; Site=2: ECO RI; Plasmid DNA from the normalized library NCI GGAP Kids prepared, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (Gnoming BSS): Subtraction by Bento Soares and M. Patima Bonaldo. "Subtraction by Bento Soares and M.
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausherg, Ph.D.
Emmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clond distribution: NCT-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/Link, send email to:
info@lmage.llnl.gov
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                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:3134372"
/lab_host="DH108"
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Location/Qualifiers
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BRail: seqrefégenoscope.cns.fr. www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10757.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI012EBGNP1&cluster=10757.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI012EE05NP1.
Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 1201)
I, W.B., Gruber.C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12927548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lib="strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 GGGGAGAAAGTGGGGATGGCTAAGAAAGCTGGGAGAAGAAGAAGAAGAAGAGGGTAGTGG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGGGCTAGGGGGGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 CAAAGATATTAAAGGCCCTGTTCATTAAGAAATTGTTCCCCTTCCCCTGTTCAATGTTTG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAAGCCCAAGCCCCAGCCCGTGGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 CTGTGTCTCCTGCCTCATCGGCCTGCCTGCAGCCAAGCCCAAGCCCAGGCCCGTGGGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAAIGITIGCCIAICCACCICCCCCAAGCCCCTTIACCIAIGCIGCIAAC---GCIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AAAGICTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAAGATATTAAGGCCCTGTTCATTAAGAATTGTTCCCTTCCCTGTGTNNAATGTNTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.0%; Score 406.2; DB 95.7%; Pred. No. 2e-95; iive 6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI012Y110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 TAAAGATTGTTCTGTGAA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
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yh12c03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone
IMAGE:43014 3' similar to contains MSR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
        166 AGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGAT 107
                                                                                                                                  106 ATTRARGECCCTGTTCATTARGARAFTGTTCCCTTCCCCTGTGTTCARGTTTGTARAGAR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 422)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             482 CCAANTITGCCTAACCACCICCCCAACCCCTTTACCTAATGCCTGCTTAAAGCTGCT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                    365 ATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCTGTGTTCAATGTTTGTAAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAAIGITIGCCIAICCACCICCCCCAAGCCCCITIACCIAIG-CIGCIGCIAACGCIGCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 492;
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84.5%; Score 394.6; DB 14; Length

Best Local Similarity 94.9%; Pred. No. 1.7e-92;

Matches 447; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                425 TGTTCTGTGTAAATATGTCTTTATAAAAAGGTG 467
                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                          TGTTCTGTGTAAATATGTTTTATAAAACAGTTAAAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:415555"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stops: 355
Source: IMAGE Consortium, LLNL
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High quality sequence stop: 363.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:43014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:830721
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R60026.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 16
R60026/c
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VERSION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., 
                                                                                                                                                                                             BE463932 406 bp mRNA linear EST 27-JUL-2000 hx83b11.x1 NCI_CGAP_Kidl1 Homo sapiens cDNA clone IMAGE:3194397 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="IMAGE:3194397"
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20 TAAAGATTGADGTGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 414)

2. Sikela,J.M.

1. Unpublished (1993)

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Seg primer: -21M13 Universal.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 AAGTGGGGGATAGCTAAGAAAGCTGGGAGATAGGGAAACAGAAGAAGGGGTAGTGGGCT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 AGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTNTTATACTAATTTTATACAAAGAT 104
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                                                                                                                                                                                                                                                           343 TITITGCCACTGACGCCCCATCAGGATTGGGCNTTNTTTCCCCCTTCCTTTNTGTGTC
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/clone_lib="Infant brain, LLNL array of Dr. M. Soares
INIB"
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83.4%; Score 389.6; DB 14; Length 414;
Best Local Similarity 97.1%; Pred. No. 3.2e-91;
Matches 403; Conservative 0; Mismatches 11; Indels 1;
       Pred. No. 1.2e-91;
); Mismatches 10; Indels
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/db_xref="taxon:9606"
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                                      393; Conservative
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   Best Local
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Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamanco, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.,
HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano, S., Isogai, T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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                                                                        GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGAACTGGTCNCCCAG 363
                                                                                                                                                                                   176
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 403)
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1618-181-3975
Fax: 81-438-52-3976
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                         GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGG-ACTGGTCGGTG-CCCAG
                                                                                                                                                                                                                                                                                                                         TCTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCCAGCCCCGTGGGGA
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                                                                                                                                                                           AAAGTCTCTTCTG-CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCC
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/note="Vector: pME18SFL3"
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/organism="Homo sapiens"
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1 (bases 1 to 396)
Hillier, L. Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Parange, C., Rikin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Parange, C., Mierry-Meg, J., Parange, C., Mierry-Meg, J., Mardis, E., Underwood, K., Mohldmann, P., Waterston, R., Wilson, R., Malson, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280,000 human expressed sequence tags (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
7441 286 1800
Fax: 314 286 1810
Email: est@wastson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (into@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham.
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                              AGTGGGTGGGCTAGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAAT
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/db_xref="GDB:3928326"
/db_xref="taxon:9606"
/clone="IMAGE:549809"
/lab_host="Nubilical vein, 1 passage"
/lab_host="Stratagene endothelial cell 937223"
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Genome Res. 6 (9), 807-828
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CENTA COT 25-NORMALIZED Homo sapiens cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
Brail: Sequencage en France
Email: sequencegensorope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10757.r For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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cgi-bin/cluster.cgi?seq=CSODI022AB12NP1&cluster=10757.r. Contact Feng Liang Bmail: fliangedlifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODI022AB12NP1.
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Whll-length cDNA libraries and normalization
Unpublished (2001)
On Peb 16, 2001 this sequence version replaced gi:12927452
                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                           Length 396;
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                                                                                                                                                                                                        82.4%; Score 384.6; DB 9;
99.0%; Pred. No. 6.5e-90;
ive 0; Mismatches 4;
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Mammalia; Eutheria; Primates;
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/lab.host="Dilog" Serim Cerr Commons. //lab.host="Dilog" CGAP GC6" //lab.host="Dilog" CGAP GC6" //lab.host="Dilog" CGAP GC6" //lab.host="Dilog" CGAP GC6" //lab.host="Dilog" CGAP GC4" was prepared, polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP GC4 was prepared, as circles were maded in vitro. Following HAP purification, so circles were maded as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470993, and 1475592-1476431.
      Clone distribution: NCI-CGAP clone distribution information can be
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_CGAP_P16 Homo Bapiens CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCTGCCACTGACGCCCCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 CAGGGATIGGGCCTICTTICCCCTTICTTICTGIGTCTCCTGCCTCATCGGCCTGCCAT
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                                    found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/hlml/iresources.shtml
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             cell tumors"
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99.7%; Pred. No. 1.-.
0; Mismatches
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                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                              clone="IMAGE:2949749"
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/mol_type="mRNA"

/db_xref="taxon:9666"
/clone="CSODIO22YC23"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGGACTGGTCGGTGCCCAGA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 recrecrecrecrecrecrivaaaeecrearecriveaereeeeacreereereereere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 TGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCAGCCCCGTGGGGAAG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 GGGAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAAACAGAAGAGGGTAGTGGG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 IGGGCTAGGGGGCCTGCCTTATTAAAGTGGT-TGTTTATGATTCTTATACTAATTTATA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 CAAAGATATTAAAGGCCCTGTTCATTAAGAAATTGTTC-CCTTCCCCTGTGTTCAATGTTT 416
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I (Dases 1 to 386)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 TGTRTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAGCCCAGCCCCGTGGGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAATGITTGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTA--ACGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                 81.5%; Score 380.6; DB 9; Length 977; Conservative 3; Mismatches 13; Indels 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 TCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTAAA 437
                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostor Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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/mol_type="mRNA"
/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
                                                                                                        AI886944.1 GI:5592108
                                                                                                                                                                                                           (human)
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// [Jab_host="Dev. | Jab_host
                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Brown
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
POLXAB-Yes.
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100.0%; Pred. No. 1e-77;
ive 0; Mismatches 0; Indels
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TAG TISSUE-placenta human full term
TAG LIB=UT-1-BBlp
TAG SEQ=AGGAA"
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/tissue_type="Placenta"
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                                                  328 GGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAA 387
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                                                                                                                                                              482 ATTGTTCCCTTCCCCTGTGTTCATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTA 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information rated to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13-21.
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/tissue_type="placenta"
/dev_stage="fetus"
/doo_lib="blacenta"
/clone_lib="blacenta"
/note="Organ: placenta; Vector: pBluescript SK-; Site_1:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                       388 ATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTA
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EST78761 Placenta I Homo sapiens cDNA, mRNA sequence.
AA167347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):172380"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 269; DB 9;
Pred. No. 1.2e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                            448 TAATAAACAGTTAAAAGCTG 467
                                                                                                                                                                                                                                                                      422 TAATAAACAGTTAAAAGCTG 403
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Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                              AA367347.1 GI:2019967
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Best Local Similarity 99.3
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 3018699423
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AA367347/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
Genoscope
Genoscope
Genoscope
Genoscope
BP 19106 EVRY codex - France
BP 1919 91006 EVRY codex - France
Bmail: seqref@genoscope.ons.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10757.r For
more information about this cluster, see
http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CSODI029CF01NF1&cluster=10757.r. Contact:
Feng Liang Bmail: fliang@lifetch.com URL:
http://fullength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI029CF01NF1.
                                                                                                                                                                                                                          EST 31-MAY-2003
                                                                                                                                                                                                                     AL571908
AL571908 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI029YL01 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db xref="taxon:966"
/db xref="taxon:966"
/clone="csopio252001292001"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo (dr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (bases I to 1200)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
92 TCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGAGATAGGGAACAGAAGAGGTAGTGGGTGGGCTAGGGGGGGCTGCCTTATTTAAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 59.7%; Score 278.8; DB 9 Best Local Similarity 76.4%; Pred. No. 5.1e-62; Matches 336; Conservative 31; Mismatches 69
                                                                     TAIGICITIAIAAIAAACAGIIAAAAGCIG 467
                                                                                            TATGTCTTTATAATAACAGTTAAAAGCTG 3
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Homo sapiens
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Best Local Similarity
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seq29-na-truncated.rst

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 334)

2 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, E.S., T., Kelley, J.M., Kelley, J.C., Lulu, L.I., Marmaros, S.M., Merrick, J.M., Phillips, C.A., Ryder, S.B., Scott, J.L., Saudek, D.M., Shirley, R., Benland, R.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Benland, K.D., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Hey, W.M., Hu, J.S., Greene, J.M., Fischer, C., Hastings, G.A., Hastings, G.A., Hastings, G.A., Hastings, G.A., Kansch, C., Hunglun, J., Hastings, G.A., Kansch, D.L., Kozak, D.L., Kunsch, C., Hunglun, J., Moissner, P.S., Olsen, H., Billion, Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, D.J., Fannon, M.R., Rosen, C.A., Haseltine, M.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                              334 bp mRNA linear EST 18-APR-1997
EST17255 Aorta endothelial cells, TNF alpha-treated Homo sapiens
ABARA16
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'clone lib="Aorta endothelial cells, TNF alpha-treated"
'note="Organ: aorta; Vector: pBluescript SK-; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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/db_xref="ATCC (inhost):116104"
/db_xref="txxon:9606"
/cell_type="endothelial cell"
/dev_stage="adult"
                                                                                                                  437 ATAIGICTITATAATAAACAGTTAAAAGCTG 467
                                                                                                                                                         31 ATAIGICTTTAINATAAACAGITAAAAGCIG 1
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The Institute for Genomic Research
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Contact: Kerlavage, AR
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AA304416
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CONA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing NCI-GCA Consortium/Library information can be
found through the I.M.A.G.E. Consortium/Library send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 292.
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3', mRNA sequence,
BF93932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 3'1; double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
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1 (bases I to 300)

NCI/NIMDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255
                                                                                                                                                       120
                                                                                                                                                                                                                                   76 crácricordecrecrizara de concaraconte de actua de concentra de contra de 
                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGAAAGTGGGGGGGATGGCTAAGAAGCTTGGGAGATTAGGGGGACCAGAAGAGGGTAGTT 315
9
                                                                       75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGG
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1 CAATGITIGCCTAICCACCTCCCCCAAGCCCCTTTACCTAIGCTGCTGCTAACGCTGCTG
                                                                       16 CAATGITIGCNIAICCACCICCCCAAGCCCCITIACCIAIGCIGCIGCIAACGCIGCTG
                                                                                                                                                       CTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGGACTGGTCGGTGCCCAGAAA
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Gaps

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56.1%; Score 261.8; DB 9; Length 334; 96.0%; Pred. No. 9.7e-58; Pred. 0; Mismatches 8; Indels 4

Query Match
Best Local Similarity 96.0
Matches 290; Conservative

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IGTTACCAATCTGAAGTGGGAGCGGCCGCATATCTTTTTT
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BF589966
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Best Local 8
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www-bio.llnl.gov/bbrp/image/image.html
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/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Al031859 409 bp mRNA linear EST 24-SEP-1998 oy45f12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1668815 3',
                                                                                                                                                                      248
                                                                                                                                                                                                                                                                                   219 GGGGGATGGCTAAGAAAGCTGGGGAGATAGGGAACAGAAGAGGGGTAGTGGGTTGGGCTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                 428
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
(CGAP/BTGAP), Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rømail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                               279 GCCNCAATGTTTGCCTATCCACCTCCCCCAAGCCCCCCCCGTGGGGAAGGGGAAAGT 220
                                                                                                                                                                                                                                                                                                                                             309 GGGCTGCCTTATTTAAAGTGGTTGTTTATGAFTCTTATACTAATTTATACAAGATATTA 368
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                      189 GCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCCAGCCCCGTGGGGAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                               369 AGGCCCTGTTCATTAAGAAATTGTTCCCTTTCCCTGTGTTCAATGTTTGTAAAGATTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 AGGCCCTGTTCATTAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTT
                                                                                                                              Gaps
  Bento
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                                                                                 Score 250.8; DB 10; Length 300;
Pred. No. 7.1e-55;
0; Mismatches 18; Indels 0;
normalized, and was constructed M.Fatima Bonaldo."
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTGTAAATATGTCTTTATAATAAACAGTTAAAAGCTG 467
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 379.
Location/Qualifiers
                                                                                                                            0; Mismatches
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:1668815"
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AI031859.1 GI:3250071
                                                                                 sch
11 Similarity 93.5%;
261; Conservative
Library is
Soares and
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Best Local Similarity
Matches 261; Conserv
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AUTHORS
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tumor Gene Index
Tumor Gene Index
Timor Gene Index
Timor Gene Index
Timor Gene Index
Timor Gene Index
Tissus Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.linl.gov
Seq primer: -40UP, from Gibco.
                           T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into Library is and Eco RI sites of the modified pT/T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
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/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCT CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF589966 229 bp mRNA linear EST 12-DEC-2000
naa33h02.xl NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258458
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 GGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGTGGGCTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                GCCTCATCGCCCTGCCATGACCTGCAGCCCAAGCCCCAGCCCCGTGGGGAAAGGAAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 AGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTT
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0
                                                                                                                                                                                                                                                            Length 409;
                                                                                                                                                                                                                                                                                                                           0; Mismatches 18; Indels
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                                                                                                                                                                                                                                                            Score 250.2; DB 9;
Pred. No. 1.1e-54;
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/db_xref="taxon:9606"
/clone="IMAGE:3258458"
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/organism="Canis familiaris"
/mol type="mRNA"
/db_xref="taxon:9615"
/clone="hd52b09"
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Location/Qualifiers
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BQ234959.1 GI:20430835
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Canis familiaris
                                                                                                                                                                                   308; Conservative
                                                                                                                                                                 Similarity
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BQ234959
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purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PGR-amplified cDNAs from a pool of 5,000 clones made from the same library (clone1Ds 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Patima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA083736 348 bp mRNA linear EST 21-OCT-1996 zn39d09.rl Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:549809 5', mRNA sequence.
                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                110
                                                                                                                                                                                                                                            Mammalia; Butheria; Primates; Catarthin; Hominidae; Homo.

(Dases I to 348)

Hillier, Lennon, Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, M., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Khucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Mortis, M., Parsons, J., Prange, C., Rikkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                       304 TAGGGGGGCCTCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGA 363
                                                                                                                                                                                                                                                                                                                                                                    423
                                                                                                                                                                                                                                                                                                                                                                                         109 TATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGA SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watgon.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28Ml3 rev2 from Amersham
High quality sequence stop: 324.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            169 TAGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTTTTTATACTAATTTATACAAAGA
                                                                                                                                                                                                                                                                                                                                                                    TATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGA
                                                                                                                                                                                   Gaps
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                                                                                                                                              47.3%; Score 220.8; DB 10; Length 229; 99.1%; Pred. No. 4.8e-47;
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                        424 TIGITCIGIGIAAATAIGICITIAIAAAAAAAGGITAAAAGCIG 467
                                                                                                                                                                                   Indels
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                                                                                                                                                              Pred. No. 4.8e-47;
0; Mismatches 2;
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                                                                                                                                                                                   Conservative
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                                                                                                                                              Query Match
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Matches 22
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S O'Shaughnessy, A.L., Palmer, L., McCombie, W.R., Baker, J.P.,

Bahret, A., Cunnius, D., Dedhia, N.N., de la Bastide, M.,

Ratzenberger, F., King, L., Kirchoff, K.A., Miller, B., Muller, S.,

Ratzenberger, F., King, L., Kirchoff, K.A., Miller, B., Muller, S.,

Nascimento, L.U., Preston, R.R., Shah, R.S., Spiegel, L.A.,

Zutavern, T., Santos, L. and Hannon, G.J.

Expressed sequence tags from Canis familiaris (dog) (5_2002)

Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8884

Email: mccombie@cshl.org

Plate: hd52 row: b column: 09

Seq primer: -21MlJJJLYREV
9
                                                                                                                                                                                                                                                                                                                                 24 CCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGC----TGCTGCTGCTGCTGCTT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 574)
                                                                                                                                                                                                                                                                                                                                                                                                                                             79 AAAGGCTCATGCTTGGAGTGGGGACTGGTC-GGTGCCCAGAAAGTCTCTTC-TGCCACTG
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                                                                                                                                                                                                                     Length 348;
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88.5%; Pred. No. 9.7e-42;
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/clone_lib="Canis Total Brain cDNAs"
/note="Vector: Lambda Zap II; The library was provided by Greg Hannon and Lee Santos (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using stratagene zap cDNA synthesis kit. It was made from dog whole brain cells. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CICITCIGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCC-CTTCCTTTCTGT 181
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Sciurognathi, Muridae, Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.Normalization and subtraction: two approaches to facilitate gene
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UI-R-BO1-aps-c-11-0-UI.S1 UI-R-BO1 Rattus norvegicus CDNA clone
UI-R-BO1-aps-c-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 GCTAGGGGGCTGCCTTATTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 GATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCC-----CTGTGTTCAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422 GATATTAAGGCCCTTTTCATTCAGAAATTGTCCCCTTCCCATAATTGTGTTCACTGTGTT
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                                                                                                                                                                                                                                                                                                                 Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 TGTAAAGATTGTTCTGTGTGTAAATATGTCTTTATAATAAAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 175.6; DB 13; Length
Pred. No. 4.6e-35;
0; Mismatches 79; Indels
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE101709.1 GI:8493807
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          Matches 298;
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                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 32
BE101709/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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COMMENT
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TITLE
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KEYWORDS
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LOCUS

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4,
clones will be available through Research Genetics (www.resgen.com) Seq primer: M13 Forward POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                 description of the library from which this clone was derived, please visit our web site at ratest.eng.ulowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIGICICCIGCCICAICGGCCIGCCAIGACCIGCAGCCAAGCCCCAGCCCCGIGGGGAAGG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GICTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCCT-TCCTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 GGACCCAGTGGGCTGTCTTATTTAAAGTGGTTGTGTATGATTCTTATACTAATTTATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 GAGATATTAAGGCCCTCTGAGTTAAAGAAACTGTCCTCATCCCGTGTGTTCACTATGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 AGGGAAGGAGGATGTTGGCTGAGAAAGAGGAGAGATAGAAACAGAAGAGGGGGAGTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGCTAGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF109372 100 799 bp mRNA linear EST 23-JUL. Shultzomica02623 Rat lung airway and parenchyma cDNA libraries Rattus norvegicus cDNA clone Contig2278 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 GGAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shultz,M.A., Zhang,L., Gu,Y.-2., Baker,G.L., Farnuchi,M.V.,
Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
Plopper,C.G. and Buckpitt,A.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 148.2; DB 10; Length 399;
Pred. No. 6.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTAAAATTGTTCCATGTAAAATATGTCTTTATAATAAAGAGGTTAAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 GTAAAGATTGTTCTGTGAAATATGTCTTTATAATAAACAGTTAAAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 graccircrigecritarcagecreeccarggecareccaeagggaagg
                                                                                              1. .399
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                            Location/Qualifiers
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TITLE

COMMENT

FEATURES

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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
FO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Enail: smitheemail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904-e. Vector identified by cross_match with the -minscore 18
POR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI901469 520 bp mRNA linear EST 12-MAR-2002 id20d03.y1 Melton Normalized Mixed Mouse Pancreas 1 N1-MWS1 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="pooled"
/lab_host="DHIOB"
/clone_lib="MHRC 3BOV"
/note="Vector: pCMV SPORT6; Site_I: NotI; Site_2: SalI;
/ibhrary made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GCCCAGCCCT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 GIGGGGAAGGGGAAAAGIGGGGGGATGGCTAAGAAAGCIGGGAGATAGGGAACAGAAGAG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 AATITATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCC----T 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404 GIGITCAAIGITTGIAAAGAITGITCTGIGTAAATATGICTTTATAATAAAACAGTTAAAA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 GTTCACTGTGTTTGTAAAGATTGTTCAGTGTAAATATGTC-TTATAATAAGAATGAAAA 327
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 GTGCCCAGAAAGTCTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GTGTCCAGAAAGCCTCTTCTGCCATGGATGCCCCCACCAGGGACTGGGCCGTTTTCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 CTTCCTTTCTGTGTCTCTGCTGCTTCATCGGCCTGCCATGACCTGCAGGCCCAAGCCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 GTGGGGAA--CGAGATGGAAGGCATGGCTGGGAAAGTCTGGGGACACGAGAAGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 GGTAGTGGGTGGGCTAAGGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 AATTTATACAAAGTTATTAAGGCCCTTTTCATTAAGAAAGCCTTCCCTTTCCCTAGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.8%; Score 130; DB 10; Length 354; Best Local Similarity 71.2%; Pred. No. 3.6e-23; Matches 259; Conservative 0; Mismatches 65; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 chrechenenerenenenenenen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 35 row: P column: 11
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 GCTG 467
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BI901469
LOCUS
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MEDLINE
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                  The sequencing and Microarray Development

L Unpublished (2003)

Contact: Shultz MA

Contact: Shultz MA

Dept. of Molecular Biosciences, School of Veterinary Medicine

University of California, Davis

1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA

Tel: 530 752 0793

Email: mashultz@ucdavis.edu

Average Phred score is 20 or better. All poor quality data (Phred < 20) and vector/linker sequence has been removed.

High quality sequence stop: 799.

Location/Qualifiers

irce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"

.Colone lib=.Rat lung airway and parenchyma cDNA libraries"
/note="Organ: lung, Vector: pGBW-11Zf(-); Site 1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 25-APR-2001
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1 (bases I to 354)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Write, J., Cho, J., Fahrenkrug, S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTTTCTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAGCCCAGCCCCGT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 GGGGAAGGGGA--GAAAGTGGGGGTGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 GGGAGTGAATGGACCCAGTGGCTGTCTTATTTAAAGTGCTTGTGTATGATTCTTATACT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA--ATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAACAGTTAAAAGCT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 CACTATGITTGTAAAAATTGTTCCATGTAAATATGTCTTTATAAAAGAGTTAAAAGCT 307
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        Expression Analysis in Response to Lung Toxicants:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14; Length 799;
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BF599804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.5%; Score 142.6; DB 14; Length 73.8%; Pred. No. 2.3e-26; Live 0; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung airways and parenchyma tissues."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'tissue_type="airway or parenchyma"
                                                                                                                                                                                                                                                                                                                                                                                              organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="Contig2278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF599804.1 GI:11696653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222; Conservative
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Bos taurus
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BF599804
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AUTHORS REFERENCE

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 520)
Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D. and Korn,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX524433 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGp998K12950; IMAGE:407171, mRNA sequence.
                       267 T------TGGCTGAGAAGAGGAGAGATAGA-AGCACAAGAGGGGGGGTAAAC 311
                                                                                                                                                                                                                                                                                                        312 gegeceaeregecrerentarinaaagregriarererarirentaraerainaran 371
                                                                                                                                                                                                                                                                                                                                                                 360 AAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCC-----TGTGTTCAAT 412
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contact RZPD (clone@rzpd.de) for further information. Seg primer:
T7, Primer seguence: TAATACGACTCACTATAGGG.
                                                                                240 GGAGAAAGTGGGGATGGCTAAGAAAGCTGGGAAGATAGGGAACAGAAGAGGGTAGTGGGT
                                                                                                                                                                                                                                                     300 GGGCTAGGGGGCCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACA
                                                                                                                                                                                                                                                                                                                                                                                                                          372 GAGATATTAAGGCCCTTTGAGTTAGAGAAACTGTCCCCTTCCCATAAGTGTGTTTCGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 GITIGIAAAGAITGIICTGIGIAAAIAIGICTITIAIAAIAACAGIIAAAAGCTG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.rzpd.de/CloneCards/cgi-
blofsbow.lib.pl.cgi/response?libNo-981 contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Fer: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RZPD Deutsches Ressourcenzentrum fuer Genomforschung
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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/dev stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
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/clone="IMAGp998K12950
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/strain="C57BL/6J"
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Unpublished (2003)
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BX524433
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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
MGI:1949994 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
                                                                                                        Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodenta; Sciurognathi; Muridae; Mus.
1 (bases 1 to 520)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrine Pañcreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                            Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marran,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Konko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Findbolished (2000)
Umpublished (2000)
Other ESTS: id20403.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:5663668"
/sex="Both for embryonic & newborn, male for adult and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn, adult, mixed"
lab host="DH10B"
/clone lib="Melton Normalized Mixed Mouse Pancreas 1 N1-MMSI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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musculus cDNA clone IMAGE:5663668 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |organism="Mus musculus"
|mol_type="mRNA"
|strain="ICR"
|db_xref="taxon:10090"
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Location/Qualifiers
                                                     BI901469.1 GI:16189020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 617-495-8557
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FEATURES		ORIGIN Query Best) Match	3 8 8 8 8 8 8 8	Qy Qy Db CF582777 LOCUS DOCUS DEFINIT ACCESSI VERSION VERYWORD SOURCE ORGAN
State Univ., from 2]; double-stranded cDNA was ligated to Bco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Bco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "	27.8%; Score 129.8; DB 13; Length 520; Conservative 0; Mismatches 87; Indels 23; Gaps GTCTCTTCTGCACTGACGCCCCATGAGGATTGGGCCTTCTTTCCCCTTTCTTT	300 GGGCTAGGGGGCTGCTTATTAAAGTGGTTGTTTATGATTCTTATACTATTTATACA 359 288 GGGCCCAGTGGGTTGTTTAAAGTGGTTATGTGTATTTCTTATACTTATTTAT	RESULT 37 B1967057 B1	Villiams, T., Jackson, Y. and Bowers, Y. Cole, K., Isagarelbillian, T., Jackson, Y. and Bowers, Y. TITLE Endocrine Pancreas Consortium Journal Oppublished (2000) CONTact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA, 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (Crown@fess harvard.edu) MGI:1950933 This sequence now available from the IMAGE consortium, for clone orders contact: info@mage.llnl.gov High quality sequence stop: 429.
S. S.	2 4 6 6 6 6	B & B & B &	RE SO SE RE	\aleph

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/note="Vector: pSPORT1; Site 1: Not 1; Site 2: Sal 1; Five libraries representing E10.5/12.5 pancreatic bud, E16.5 pancreas, and adult plancreas, and seperately constructed using superScript Plasmid Library kit (Life Technologies). CDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on Solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonalod, Lennon, and Soares normalized by method #4 from Bonalod, Lennon, and Soares 1996 Genome Research 6:791-806, 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:5664607"
/sex="Both for embryonic & newborn, male for adult and
adult islet"
                                                                                                                                                                                                                                                 /dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn, adult, mixed"
/lab_host="DH10B"
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69.0%; Pred. No. 4.6e-23;
.ive 0; Mismatches 87; Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                          /clone_lib="Melton Normalized Mixed Mouse Pancreas 1 N1-MMSI"
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Mus musculus
                                                                                            /mol_type="mRNA"
/strain="ICR"
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Local Similarity 69.0*
hes 245; Conservative
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SOURCE

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/note="Organ: pancreas; Vector: pSPORT1; Site 1: Sall; Site_2: NotI; Library consists of a pool of clones rearrayed from the following libraries: Melton normalized mixed mouse pancreas 1 NI-MMS1, Amplified Melton mouse islets 1 MIS1-A, and Kaestner ngn3 wt. Clones rearrayed in the laboratory of K. Kaestner (University of Pennsylvania). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 T------TGGCTGAGAAAGAGGAGATAGA-AGCACAAGAGGGGAGTAAAC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 GGGCTAGGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTTATACA 359
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                                                                                                                                                                                                                                                                                                                  COUNT Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Rlate: IRBD26 row: g column: 10
High quality sequence start: 22
High quality sequence stop: 705.
                                                                                                     Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gow
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GTCTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCT-TCCTTTCT
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                                                  National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="IMAGE:6432441"
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Best Local Similarity 69.09
Matches 245; Conservative
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Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

Wray, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

FOD Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4356

Fax: 402 762 4390

Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                               Single pass segmencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.

Plate: FQY8034 row: I column: 3
Seg primer: GTAATACGACTATATAGGG.
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                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 CGGTGCCCAGAAAGTCTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 CTGTGGGGAA--CGAGATGGAAAGGGATGGCTGGGAAAGTCTGGGGAACACACGAGAAGT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 CTAATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 CIAATTITATACAAAGTTATTAAGGCCCTTTTCATTAAGAAAGCCTTCCCTTTCCTAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.7%; Score 125.7,
70.8%; Pred. No. 6.2e-23;
itive 0; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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'db_xref="GI:26334911"
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Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 GTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCCAGCCCCGTGGGGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="unnamed protein product; APELIN PRECURSOR (APJ ENDOGENOUS LIGAND) (SWISSPROT|Q9R0R4, evidence: FASTY, 100%ID, 100%length, match=231)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2266 gecricircracrecregraceceraceassascessecricircescerringies representation
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                                                                                                   Please visit our web site for further details.
URL.http://ganome.gsc.riken.go.jp/
URL.http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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ilarity 68.9%; Pred. No. 1.4
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsuncto, H., Zakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Murametcu, M., Inoue, Y., Kira, and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
wehr. Enzymol. 303, 19-44 (1999)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 780)
                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Lochar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LiAMI1370 row: j column: 21
High quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 CCCCATCAGGGATTGGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCATCGGCC
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                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.2%; Score 127.2; DB 12; Length 780;
68.6%; Pred. No. 2.5e-22;
tive 0; Mismatches 83; Indels 22; Gaps
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/clone="IMAGE:5149940"
/clssue_type="tumor, gross tissue"
/dev_stage="7" months"
/lab_host="DH108"
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/organism="Mus musculus"
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/strain="C57BL/6J"
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BX118770
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596 bp mRNA linear EST 15-OCT-1996
zd38f03.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone
IMAGE:342941 5', mRNA sequence.
W67823
W67823.1 GI:1376742
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free from RZPD; contact RZD; conteact RZD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                   Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuthelmer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 TCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCC
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RZPD; IMAGP998G06783.

Ruman UnigeneSet - RZPD3 (RZPDLIB NO.972)

http://www.rzpd.de/CloneCards/Cg1-

http://www.rzpd.de/CloneCards/Cg1-

blinfshow.Lib.pl.cgi/response7libNo-972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Far: +49 30 32639 101

Fax: +49 30 32639 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998G06783 ; IMAGE:342941"
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100.0%; Pred. No. 2.5e-22;
tive 0; Mismatches 0;
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/organism="Homo sapiens"
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Best Local Similarity 100.
Matches 127; Conservative
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Dubuque, T.,
                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 486)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Gaesel,S., Kucaba,T., Lacy,M., Lac,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GICTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCT-TCCTTTCT 179
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                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 AAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCC-----TGTGTTCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                          Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1395365.
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
H44 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 484.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:407171"
/sex="unknown"
                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
  musculus (house mouse)
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243; Conservative
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                       Mus musculus
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Matches 243; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double-stranded cDNA was size selected, ligated to Eco RI additions of the More and addition and all and cloned into the Not I and Eco RI sites of a modified pT/T3 vector (Pharmacia). Library went through one round of mormalization to a Cot = 5. Library constructed by M. Ratina Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 TCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTGTGTTTCAATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAACAGTTA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAAACAGTTA 120
                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 630 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTATACTAATTTATACAAAGATATTAAAGGCCCTGTTCATTAAGAAATTTCTTCCCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                    1 (bases 1 to 596)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                    The WashU-Merck EST Project Unpublished (1995)
Unpublished (1995)
Contact: Wisson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.2%; Score 127; DB 14; Length 596; 100.0%; Pred. No. 2.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1268316"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 394.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:342941"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W84234.1 GI:1541218
sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .596
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                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                  ORGANISM
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VERSION
KEYWORDS
                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
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                                                                                    REFERENCE
                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
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SOURCE
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4;

299

5

Gaps

22;

Length 449;

344

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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
FO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4360
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                               345 ATACTAATTTATACAAAGATATTAAGGCCCCTGTTCATTAAGAAATTGTTCCCTTCCCC-- 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 ATACTAATTTATATÁGAGATÁTTAAGGCCCTTTGAGTTAGAGAAACTGÍCCCCTTCCCAT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 AAGTGTGTCGCTATGTTTTAAAAATTCTTCCATGTAAATATGTCTTTATAATAAAGAG 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae, Bovinaer, Bos.

1 (bases 1 to 342)

2 Smith, T.P. L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., Mhite, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, W.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Fertea, G., Holt, I., Karamycheva, S., Liang, F., Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 ACAGGGAAAGGGAGGGGGAATAT-----TGGCTGAGAAAGAGGAGAGAGATAGA-AGCAC
                                                                                                                                                                                                                                                                                                                        166 CCCCCT-TCCTTTCTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 GCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 AAGAGGGTAGTGGGTGGGCTAGGGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 AAGAGGGGAGTAAACGGGCCCAGTGGGCTGTCTTATTTAAAGTGGTTATGTGTATTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTAATAAACAG
                                                                                                                                                                               106 GTCGGTGCCCAGAAAGTCTCTTCTGCCACTGACGCCCCCCATCAGGGATTGGGCCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                            155 GTCTTTGTCGTTTCTGCACCTCCTTCCTTATCAGCCTGCCATG-----GCCAGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         br600467 342 bp mRNA linear 265082 MARC 3BOV Bos taurus cDNA 5', mRNA sequence. BF600467
                          Score 124.2; DB 10; Length
Pred. No. 1.3e-21;
0; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACKWARD: GTTTTCCCAGTCACGACG
Plate: 37 row: P column: 11
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                      Query Match
Best Local Similarity 68.7'
Matches 252, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 TTAAAAG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 TTAAAAG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11282978
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ACCESSION
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SOURCE
ORGANISM
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BF600467
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Cénter (620), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9216
Fax: 81-45-503
Fax: 81-45-503
Fax: 81-45-503
Fax: 81-45-503
Fax: 81-45-503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E. (Dases I to 449)
E. (Dases I to 449)
Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K.,
Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N.,
Sagaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, R., Takaku-Akahira, S.,
Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length CDNAS (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing pipeline with 384 multicapillary system. -384-IOTMAT 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                        EST 19-NOV-2001
346 GAGATATTAAGGCCCTTTGAGTTAGAGAAACTGTCCCCTTCCCATAAGTGTGTACGCTAT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="mammary gland"
/cell line="RCB-0526 Jyg-MC(A)"
/clone lib="RIKEN full-length enriched, mammary gland
/CB-0526 Jyg-MC(A) cDNA"
                                                                                                                  RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                          BB819942 RIKEN full-length enriched, mammary gland RCB-0526 Jyg-MC(A) cDNA Mus musculus cDNA clone G830003B15 3', mRNA
                                                                        GTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAAGCTG
                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="G830003B15"
                                                                                                                                                                                                                                                                                                                            449 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB819942.1 GI:16992571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse tissues.
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                                                                                                                                                                                                                                                       RESULT 45
                                                                                                                                                                                                                                                                              BB819942
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
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EST 25-APR-2001

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Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Analysis of bovine mammary gland EST and functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATGITIGITIAAAAGAITGITICIGIGIAAAAAGGICTIAIAAAAAAAAGATAAAAAGAGTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410 AATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAACAGTTAAAAGCTG 467
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1 (bases 1 to 480)
Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@inage.llnl.gov) for further information.
Insert Length: 720 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 451.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 AATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.3%; Score 118; DB 14; Length 616; 100.0%; Pred. No. 6e-20; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brz31395 480 bp mRNA linear
253781 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.
Br231395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Sonstegard TS
VSDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Bos taurus gene index Mamm. Genome 13 (7), 373-379 (2002) 22135956
                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="GDB:1323684"
/db_xref="taxon:9606"
/clone="IMAGE:415214"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF231395.1 GI:11170359
                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 118; Conservative
                                                                                                                                                                                       .616
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VERSION
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COMMENT
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2h47c08.rl Soares fetal liver spleen INFLS_S1 Homo sapiens CDNA clone IMAGE:415214 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345
                                                                                                           /clone_lib="WARC 3BOV"
/note="Vector: pCMV SPORT6; Site_l: Notl; Site_2: Sall;
/instary made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                         106 GTCGGTGCCCAGAAAGTCTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 CCCCCTTCCTTCTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCAG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- GCCCAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCCGTGGGGAAGGGGAAAGTGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTGTGGGGAA--CGAGATGGAAAGGGATGGCTGGGAAAGTCTGGGGACACGAGAAGT- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------dagangcraadagacraritatritaaagracraraahritaa 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 TACTAATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCC--- 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 AACTAATTTATACAAAGGTATTAAGGCCCTTTTCATTAAGAAAGCCTTCCCTTTCCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTTATAATAACAGTT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 TIGIGCTCACTGTGCTGGTAAAGATTGTTCACTGTAAATATGTC-TTATAATAAAGAATG 333
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1 (bases 1 to 6.6).
1 Hillar, L. Lemon, G. Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Mardis, E., Morre, B., Morris, M., Parsons, J., Prange, C., Rikin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Travaski, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                      8 GGCAGTGTGTGAAAGCCTCTTCTGCCATGGATGCCCCCACCAGGGACTGGGCCGTTTTC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                               25.3%; Score 118; DB 10; Length 342; 68.8%; Pred. No. 4.9e-20; ive 0; Mismatches 75; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                      /clone lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled mENA isolated from mammary
tissues at eight physiological, developmental, and disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Э,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 GGGACTGGGCCGTTTTCCCCTTTCCTCTCTGCTTCTCCTGTCGCATCAG----- 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 CCTGCAGCCAAGCCCAGCCCCGTGGGGAAAGGGGAAAAGTGGGGAATGGCTAAGAAAGCT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TTGCCCAGCCCTGTGGGGAA--CGAGATGGAAAGGGATGGCTGGGAAAGTC 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTTGGAGTGGGGACTGGTCGGTGCCCAGAAGTCTTCTGCCACTGACGCCCCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 GGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae;
I (bases 1 to 921)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                         25.2%; Score 117.8; DB 10; Length 69.6%; Pred. No. 6.2e-20; ive 0; Mismatches 62; Indels
                                                                                                                                                                      organism≈"Bos taurus"
                                                                                Plate: 105 row: I column: 14
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
                                        FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GITTTCCCAGTCACGACG
                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
-minmatch 12 options.
PRimers
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Best Local Similarity 69.6
Matches 218; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 TIGITCCCTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
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AUTHORS
TITLE
JOURNAL
COMMENT
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LOCUS
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EMEATORIAS ELECTRONAGE CRANIATA, Vertebrata; Euteleostomi, Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.

E (Bases 1 to 231)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
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/tissue_type="tumor, gross tissue"
/dav stage="r months"
/lab_host="nH108"
/clone_lib="NGI_GGAP_Mams"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 GAG-GGGGAATATTGGCTGAGAAAGAGGAGATAGA-AGCACAAAAAGAGGGGAGTAAACG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GCTAGGGGGCCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCC-----TGTGTTCAATG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TCCTGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAAGCCCGGTGGGGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 24.8%; Score 115.8; DB 12; Length 921; Best Local Similarity 69.9%; Pred. No. 2.6e-19; Matches 248; Conservative 0; Mismatches 87; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 GCCTCTTCTACTGCTGCTACCCTACCAGGGACCGGGCCTTC
                                                                                row: k column: 13
                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
http://image.llnl.gov
Plate: LLAM11651 row: k col
High quality sequence stop: 6
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                   Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGGTCTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 CCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAAGGCCC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 TCTTATTTAAAGTGGTTATGTGTATTTCTTATACTAATTTATAGAGATATTAAGAGCCC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 IGITCATIAAGAAATTGTTCCCTTCCCC-----TGTGTTCAATGTTTGTAAAGATTGT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /noce="Site 1: Sal1; Site_2: BamH1; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp/
URLsaski,N. Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 TGTCTAAGAAAGAGGAGAGATA-GAAGCACAAGAGGGGAGTAAACGGGCCCAGTGGGCTG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="RIKEN full-length enriched, 16 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Gaps
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     RIKEN Mouse ESTs (Konno, H., et al. 1999)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="lung"
'dev_stage="16 days embryo"
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:10090"
clone="8430414M03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mol_type="mRNA"
|strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="mixed?
                                                                                                                                                                                                                          Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity '*..
Matches 164; Conservative
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TITLE
JOURNAL
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132 TTTGAGTTAGAGAAACTGTCCCCTTCCCATAAGTGTGTTCGCTATGTTTGTAAAAATTGT 191
                                                                  428 TCTGTGTAAATATGTCTTTATAATAACAGTTAAAAGCTG 467
                                                                                                           192 TCCALGTAAATATTTTTTATAATAAAGAGTTAAAAGTTG 231
임
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completed: May 25, 2004, 17:18:12 Ne : 2869 secs

5 414 88 6 384 82 7 373 79 8 370 79	10 347 74	Search time 2864 Seconds	C 15 291 62 285 61 C 17 242 51 C 17 242 51 C 18 C 17 242 51 C 17 C 18 C 18 C 18 C 18 C 18 C 18 C 1	.0 c 21 241 51	0276 residues c 23 205 43	24 201 43 25 197 42	parameters: 13639910 c 27 156 33 c 28 155 33	29 132 28 30 127 27	31 127 27 32 118 25	71 18 71 18	35 75 16 36 61 13	52 11	40 41 8 41 34 7	42 30 6	7 50 6	757	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	50 228 6	722 288 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	27 52	56 27 5	58 27 5	60 27 5	62 27 5	ts nyadinted by chance to barre a	to granted being printed, c 66 27 5 e total score distribution.	68 27 5 69 27 5	71 27 5	5075 BM975075 UI-CF-ECI C 774 27 5.8 981 AI149981 qf38h10.x C 75 27 5.8 212 AW015212 UI-H-BIOp 76 27 5.8 4588 CA444588 UI-H-DII- C 77 27 5.8
GenCore v Copyright (c) 1993 -	OM nucleic - nucleic search, using sw	Run on: May 25, 2004, 17:18:40	Title: SEQ29-NA-TRUNCATED Perfect score: 467 Sequence: 1 caatgtttgcctatccacct	Scoring table: OLIGO_NUC Gapop_60.0 , Gapext 60	Searched: 27513289 seqs, 1493109	Word size : 10	Total number of hits satisfying chosen	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Listing first 100 sum	EST:*	1: em_estba:* 2: em_estbam:* 3: em_estbam:*	E E	6: em_estpl:* 7: em_estro:*	8: em_htc:* 9: gh est1:*	10: 90 est2:* 11: qb htc:*	12: gb_est3:* 13: qb_est4:*	14: gb_est5:* 15: em_estfun:*	16: em_estom:* 17: em_gss_hum:*	e m		e e	em gss	em_gss_ em_gss_		go_gssz:" The number of resul	s greater than or equal to t is derived by analysis of th	SUS	Result Query No. Score Match Length DB ID	C 1 466 99.8 728 12 BM775075 C 2 447 95.7 450 9 AI149981 C 3 414 88.7 449 9 AW015212 C 4 414 88.7 517 14 CA444588

BQ006616 UI-H-EII-BBE5577 7910e01.x
BX434223 BX434223
AA09445 ZA8B577.T
CA448256 UI-H-DTI-AI871469 w167d09.x
AW594286 h657h03.x
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BF222471 hr75g11.x
AI86694 w194d03.x
BR65392 nac64d01.
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AI031859 0745f12.x
AA083737 za39406.s
AA101878 ZA85f07.s
AA367347 EST77251
AA57734 AL570843
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AA101878 ZA85f07.s
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AA367347 EST77261
BF58996 ma33h02.s
AA101878 ZA85f07.s
AA083737 za39409.r
AA367347 EST77237
AA65823 ZA66609.r
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BF58996 LD-H-DTO-BQ006379 UI-H-EII-BQ23805 CCA27694
BF114974 MF7204.x
AA083736 ZA959 H65500.g
AA367347 EST73237
AA66831 F06500 T
BF58996 LD-H-DTO-BQ006379 UI-H-EII-BQ23896 ECCA27694
BC528108 602557488
BC66891 HV CEa001
BF58938 BY479938
BF766891 HV CEA001
BF589384 EST73237
AA05531 F06500 T
BC5231 F06500 T
BC52474 BC776745 ECCA2764
BC523676 WM51 F608
CD343253 EEESTEE67
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AA55006 LD30941.5

/dev_stage="Adult and Fetal" /lab_host="DH108 (Life Technologies) (T1 phage resistant)" /clone_lib="UT-CF-EC1" /clone_lib="UT-CF-EC1" /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site=1: EcoR I; Site=2: Not I; UT-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligomicacide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC. TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383 TAG_LIB=UI-CF-ECI TAG_SEQ=AAGTGCTTAC.	Query Match 99.8%; Score 466; DB 12; Length 728; Best Local Similarity 100.0%; Pred. No. 1.2e-221; Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 CAATGTTTGCCTATCCACCTCCCCAAGCCCTTTACCTATGCTGCTAACGCTGCTG 60 484 CAATGTTTGCCTATCCACCTCCCCCAAGCCCTTTACCTATGCTGCTGCTAACGCTGCTG 425 61 CTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	to contains element FTK5 repetitive elem GI:3678450 S (human) S Metazoa; Chordata; Craniata; Vertebrata;
10 AW678825 AW678825 WS1 1 F08 12 BIG38657 SD21007.5 14 CD825475 BIG38657 SD21007.5 15 SB21757 BR25.0600 15 BE31757 BR25.0600 20 CW3020KB AL17570 Tetracdon 22 BH719045 CG56374 MBERBIZOTR 23 CW5030H2 AL125223 Tetracdon 24 CW5030H2 AL125729 Tetracdon 25 CW5030H2 AL155759 Anopheles 13 BU716281 BB023936 BB023936 BB023936 24 CD56591 BB023936 BB023936 25 AL284913 AL256810 UL25f1.y 26 CM5030H2 AL256810 UL25f1.y 27 CM49837 CG449837 Hd mx18 0 28 AU255321 BW255321 AU25532 29 AU37552 AU37522 20 AU37552 AU37522 20 AU37552 AU37522 21 BF468581 CG343156 ELEGTee76 22 AU355366 ELEGTee76 23 AU37554 AU375346 24 CD343166 BJ475346 26 AZ006229 RPCI-23-3	ALIGNMENTS	DW975075 UI-CF-ECI-acf-1-23-0-UI.sl UI-CF-ECI Homo sapiens CDNA clone UI-CF-ECI-acf-1-23-0-UI 3', mRNA sequence. UI-CF-ECI-acf-1-23-0-UI 3', mRNA sequence. BM9775075.1 GI:19592666 BM9775075.1 GI:19592666 BM9775075.1 GI:19592666 BM977675.1 GI:19592666 BM977675.1 GI:19592666 BM977675.1 GI:19592666 BM977675.1 GI:19592666 BM977676.1 Mctazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 728) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 728) Normalization and subtraction: two approaches to facilitate gene discovery Genome Res. 6 (9), 791-806 (1996) 97044477 97044477 97044477 PM97 ACC TOWA 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Fax: 319 356 4866 Fax: 319 356 4171 Email: paul-mccray@riowa.edu CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CLONE DISCLIBULION: Researchers may obtain clones from Research CLONE DISCLIBULION: Researchers may obtain clones from Research (www.openbiosystems.com) The following repetitive elements were found in this CDNA Sequence: 408-444, > (CAG)n#Simple_repeat (Matched compliment) PONYMALES. SEQUENCE: M3 FORMARD	Location/Qualifiers 1728 /organism="Homo sapiens" /organism="Homo sapiens" /mol_mana, /db_xref="taxon:9606" /clone="UI-CF-ECI-acf-1-23-0-UI" /tissue_type="Lung"
C 78 27 5.8 627 C 80 27 5.8 639 C 81 27 5.8 736 82 27 5.8 818 84 27 5.8 816 C 86 27 5.8 816 C 87 27 5.8 816 C 88 27 5.8 816 C 92 27 5.8 915 C 92 26 5.6 217 C 93 26 5.6 284 C 94 26 5.6 284 C 97 26 5.6 310 C 98 26 5.6 310 C 99 26 5.6 310 C 99 26 5.6 310 C 99 26 5.6 310 C 100 26 5.6 317		RESULT 1 BM975075/ LOCUS LOCUS LOCUS LOCUS UI-CF-ECI-acf-1-23-0-UI.S UI-CF-ECI-acf-1-23-0-UI.S UI-CF-ECI-acf-1-23-0-UI.S UI-CF-ECI-acf-1-23-0-UI.S UI-CF-ECI-acf-1-23-0-UI.S UI-CF-ECI-acf-1-23-0-UI.S UI-CF-ECI-acf-1-23-0-UI.S BM975075 BM975075 BM975075 HOMO sapiens EUKATYOCES HOMO sapiens EUKATYOCES HOMO Sapiens UKATYOCES HOMO SACORT OF THE SAUTHORS UCANALLY BORALINE HOMO SACORTY GENOMENT CONTACT: MACCTAY, PEB WCCTAY LAB UNIVERSITY OF IOWA M TOLING PROSTITY ATTAYOR DIA TOLING PROSTITUTY ATTAYOR DIA CONDA LIBRATY CONDA LIB	FEATURES Location/ Source 1728 / Organism / mol_type / db xref= / clone="type" / tissue_t

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gex="male"
/lab host="DHIOB"
/lab host="DHIOB"
/clone lib="Soares testis NHT"
/note="Wector: pr7T30-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                 Sequencing Center information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.
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1 (Dassa 1 to 450)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Double-stranded cDNA was ligated to Eco RI adaptors
                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                 CDNA Library Arrayed by: Greg Lennon, Eh.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.B. Consortium/Linn at:
                                                                                                                                                                                                                                                                                                                               www-bio.linl.gov/bbrp/image/fmage.html
Insert Length: 718 Std Error: 0.00
Seg primer: -40ml3 fwd. Err from Amersham
High quality sequence stop: 417.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
                                                                                              Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: capbs-remail.nih.gov.
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares lab Clone distribution: NCI.CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                   EST 10-SEP-1999
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1 (bases 1 to 449)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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www-bio.llnl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 408-447,
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                                                                                                                                                                                                                                       linear
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UI-H-BIOD-aba-e-12-0-UI.s1 NCI_C
MAGE:2711158 3', mRNA sequence.
                                        30 GTCTTTATAATAACAGTTAAAAGCTG 4
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Location/Qualifiers
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Seg primer: M13 Forward
POLYA=Yes.
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AW015212.1 GI:5863899
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AW015212/c
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Figure Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 409-448, > (CAG) n#Simple_repeat
POLYA-Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA444588 517 bp mRNA linear EST 08-NOV-2002
UI-H-DT1-awl-m-06-0-UI.s1 NCI CGAP DT1 Homo sapiens cDNA clone
UI-H-DT1-awl-m-06-0-UI 3', mRNA sequence.
   To Facilitate Gene Discovery.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                        CAGAAAGTCTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTC
                                                                                                                                                                                          GCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAACAGTTAAAAGCTG
                                                                                                                                                              0;
                                                                                                                           Score 414; DB 9; Length 449;
                                                                                                                                                             Indels
                                                                                                                                        1.le-195;
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Subtraction: Two Approaches
Genome Research 6, 791-806.
TAG_TISSUE-brain
TAG_LIB=NCI CGAP_Brn23
TAG_ESQ=ATATC"
                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
                                                                                                                                              Pred. No.
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                                                                                                                      88.7%; Sccilarity 100.0%; Pr
Conservative 0;
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CA444588.1 GI:24809008
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                                                                                                                                          Similarity
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/dev stage="Addit"
/lab_host="DH10B (Life Technologies)"
/clone lib="MCI CGAP DT1"
/note="Organ: Ling; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP DT1 is a normalized cDNA library containing the following tissue(s): Metatastic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligomuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGTTCGG.
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 668)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 CCAGAAAGTCTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 CTTTCTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 GCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 CTITCTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAGCCCCGTGG
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UI-H-EII-aza-n-02-0-UI.s1 NCI CGAP_EI1 Homo sapiens CDNA clone
BQ006616
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TAG_LIB=UI-H-DT1
TAG_SEQ=AACTGTTCGG"
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                            type="Metastatic Chondrosarcoma"
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/clone="UI-H-DT1-awl-m-06-0-UI"
/tissue_type="Metastatic Chondro
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Mammalia, Butheria, Primates,
1 (bases 1 to 668)
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Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoolinage.lln.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 472.
                                                                                                                                                                                                                           BE855577 555 bp mRNA linear EST 29-SEP-2000 7910e01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3306072 3' similar to contains element OFR repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CIGCIGCIGCIGCITAAAGGCICAIGCIIGGAGIGGGGACIGGICGGIGCCCAGAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 552)
NCI/MINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Siscades and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BIGAP), Thmor Gene Index Unpublished (1998)
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             TTTGTAAAGATTGTTTCTGTGTAAATATGTCTTTATAATAAAAGGTTAAAAGCTG 19
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384; Conservative 0; Mismatches
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/organism="Homo sapiens"
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Homo sapiens
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Best Local S:
Matches 384,
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                                                                                                                                         RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / taw_inver="unitud (unite Technologies)"
/clone_lib="NGI_CGAP_EII"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: BcoR I; Site_2: Not I;
NGI CGAP_EII is a normalized cDNA library containing the
following tissue(a): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonuclectide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT).18 tail. The sequence tag for this library is
                                                                                                         Email: cgapbs-remail.nl.gov
Trissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M Bento Soares, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LiML at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
Seq primer: M13 FORWARD
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAGGGAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGAGGTA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGGTGGGCTAGGGGGCTGCCTTATTAAAGTGGTTGTTTATGATTCTTATACTAATT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.7%; Score 414; DB 12; Length 6t 100.0%; Pred. No. 1.2e-195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:5846209"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B_(Life_Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-EI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .668
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG SEQ=ACACTTGCAC"
                           Unpublished (1997)
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Best Local S:
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zk85f07.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone
IMAGE:489637 5' similar to contains element PTR5 repetitive element
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                             Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 431)
Hillar,L., Lemnon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Rohling,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Weg,J.,
Treyaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clome_lib="Soares_pregnant_uterus_NbHPU",
/note="Argan: uterus; Vector: pT/T3-Pac; Site_1: Not I;
Site_2: Eco Et; 1st strand cDNA was primed with a Not I
oligo(dr) primer [5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                             TGTCTCCTGCCTCATGGCCTGCATGACCTGCCAAGCCCAGCCCCGTGGGGAAGGG
                                                                                                                    241 GAGAAAGTGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTG
                                                                                                                                                              222 GAGAAAGTGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGGTAGTGGGTG
                                                                                                                                                                                                         GGCTAGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 528 Std Error: 0.00 Seq primer: -28N13 rev2 from Amersham.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                   361 AGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAA
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AACTGGAAGAATTGGGGGCGGCCTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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mol_type="mRNA"
db_xref="dDB:3804224"
/db_xref="taxon:9606"
/clone="IMAGE:489637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 bp
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/lab_host="DH10B"
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AA099445.1 GI:1645393
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/tissue type="PLACENTA"
/tissue type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
    229
                                                 300
                                                                                            169
                                                                                                                                  GGCTAGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAA 360
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BP 191 91006 EVRY cedex - France
Email: Sequencope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10757.r For
more information about this cluster, see
http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CSOBAK025CH09NM1&cluster=10757.r. Contact
Feng Liang Email: fliangalifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAK025CH09NM1.
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1. (bases 1 to 889)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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TGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCCAGCCCCGTGGGGAAGGG
                                          GAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGGTAGTGGGTG
                                                                                228 GAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAAACAGAAGAGAGGGTAGTGGGTG
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/db_xref="taxon:9606"
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Matches 423; Conserv
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Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
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(Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pr773 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 687)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                  10 CTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTAACGCTGCTGCTGCTGCTGCTGCTGCT
                                                                                                                                                            CTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCTGCTGCTGC
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. NCI_CGAP_DT1 Homo sapiens cDNA clone
                                                                                                                                Gaps
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The following repetitive elements were found in this cDNA
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                0;
                                                                                                 Length 431;
                                                                             Score 370; DB 9; Lengtn *...
Pred, No. 1.1e-173;
...arches 1; Indels
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UI-H-DT1-avw-g-05-0-UI 3', mRNA sequence.
                                                                                  79.2%; Scor.
99.8%; Pred. No. 1.1.
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Unpublished (1997)
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/dlone="Ul-H-DTI-avw-q-05-0-Ul"
/tissue type="Metastatic Chondrosarcoma"
/dev_stage="Metastatic Chondrosarcoma"
/dev_stage="Metastatic Chondrosarcoma"
/dev_stage="Metastatic Chondrosarcoma"
/lab_host="Holio Ulife Technologies)"
/clone lib="NCI CGAP DTI"
/note="Uorgan: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
NCI CGAP DTI is a normalized cDNA library containing the following tissue(s): Metastatic Chondrosarcoma in Lung.
The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this
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TAG LIB=UI-H-DT1
TAG SEQ=AACTGTTCGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.7%; Score 363; DB 14; 99.8%; Pred. No. 3.6e-170; iive 0; Mismatches 1;
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organism="Homo
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1409 Std Exror: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 450.
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                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 482)
NCI/NINDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
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                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                                                                                                                                                                                                                                                                                1. .482
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/ note="Vector: pT7150-pac (Pharmacia) with a modified
/ note="vector: pT7150-pac (Pharmacia) with a modified
/ note="weator: pT7150-pac (Pharmacia) note:"weator: pT7150-pac (Pharmacia) note="weator: pT715
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hg57h03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2949749 3',
mRNA sequence.
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CSAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
image.llnl.gov/image/hmi/iresources.shtml
Seq primer: -40UP from Gibco.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                48 AGGITGTTCTGTGTAAATATGTCTTTATAATAAACAGTTAAAAGCTG
420 AAGATTGTTCTGTGTAAATATGTCTTTATAATAAACAGTTAAAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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Tumor Gene Index
Unpublished (1997)
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Best Local Similarity
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                                                            250
                                                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                             RESULT 13
BF222471/c
LOCUS
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TITLE
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KEYWORDS
SOURCE
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Tissue Procurement: Dr. Steven Brown
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
                                                                                                                                                              EST 27-MAR-2002
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   386
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1 (bases 1 to 356)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                             CGAP_P16 Homo sapiens cDNA clone
               146 TGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGGCCCTGTTCATTAAGA
327 IGGITGITIAIGAITCITAIACTAAITTAIACAAAGAIAITAAAGGCCCIGITCAITAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                       387 AATTGTTCCCTTCCCTGTGTTCAATGTTTGTAAAGATTGTT 428
                                                                     86 AATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG TISSUE=placenta human full term
TAG LIB=UI-1-BB1p
TAG SEQ=AGGAA"
                                                                                                                                                           BQ024597
UI-1-BB1p-aus-e-04-0-UI.S1 NCI CGAP P16 Hor
UI-1-BB1p-aus-e-04-0-UI 3', mRNA seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: M13 FORWARD POLYA=Yes.
                                                                                                                                                                                                     BQ024597
BQ024597.1 GI:19759876
                                                                                                                                                                                                                                                   sapiens (human)
                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 338; Conservative
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                    Homo
                                                                                                                                          BQ024597/c
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                                                                                                                            RESULT 12
                                                                                                                                                                                                     ACCESSION
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KEYWORDS
                                                                                                                                                                                                                                                                                                            REFERENCE
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/lab host="DH10B"
/clone lib="NUI CGAP_Kid11"
/clone lib="NUI CGAP_Kid11"
/clone lib="NUI CGAP_Kid11"
/note="Grgan: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NUI CGAP_Kid3 was prepared, and ss circles were made in vitro: Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was FCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDB 1322376-1323911, 1456007-1456775, and 1500552-1502655). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissaue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissaue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lemnon, Ph.D.

CDNA Library Arrayed by: Greg Lemnon, Ph.D.

Clone distribution: NG-Schoor distribution information can be found through the I.M.A.G.E. Consortium/LLML, send email to: info@image.llnl.gov

High quality sequence stop: 416.
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249
                                               177
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                                                                                                                                                                                                                                                                                                                                                                        176 GGCTGCCTTATTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 GGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF222471 428 bp mRNA linear EST 09-NOV-200 hr75g11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134372 3' similar to contains element OFR repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 428) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
190 CCTCATCGGCCTGCCATGACCTGCAGCCCAGCCCCCGTGGGGAAGGGGAAAGTG
                                                                                                                                              GGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGGTGGGGTGGGCTAGGGG
                                                                                                                                                                                                                      310 GGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430 TGTGTAAATATGTCTTTATAATAAACAGTTAAAAGCTG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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198 281

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Bumert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8E463932 LOJUL-2000
bx83b11.x1 NCI_CGAP_Kidl1 Homo Sapiens cDNA clone IMAGE:3194397 3',
                                                                                                                                                    GCTGCTAAACGCTGCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 CAAAAAGGGTAGTGGGTGGGCTAGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402 CIGIGIICAAIGIIIGIAAAGAIIGIICIGIGIAAAIAIGICIIIIAIAAIAAACAGIIAA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 406)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 CTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATAATGTCTTTATAATAACAGTTAA
                                                                                                                       42 GCTGCTGCTAACGCTGCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGG
                                                                                                                                                                                                                ACTGGTCGGTGCCCAGAAAGTCTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTT
                                                                                                                                                                                                                                          377 ACTGGTCGGTGCCCAGAAAGTCTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTT
                                                                                                                                                                                                                                                                                                        CTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAAGC
                                                                                                                                                                                                                                                                                                                                          317 CTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGC
                                                                                                                                                                                                                                                                                                                                                                                              222 CCAGCCCCGTGGGGAAGGGGAGAAGTGGGGGATGGCTAAGAAAGCTGGGAAGATAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                         257 CCAGCCCCGTGGGGAAGGGGAGAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 CAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCTTATTTAAAGTGGTTGTTTATGATT
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0
                                   Length 437;
                                                                            2; Indels
                                 Score 324; DB 9;
Pred. No. 1.1e-150;
0; Mismatches 2;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab host="DH10B"
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                                 tch 69.4%;
al Similarity 99.5%;
424; Conservative
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Unpublished (1997)
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BE463932
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                               Query Match
Best Local S:
Matches 424
                                                                                                                                                                  437
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BE463932/c
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones ande from the same 3 libraries. The pools
consisted of I.M.A.G. clones 260232-265223,
340488-345479, and 484488-489479."
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                                                                                                                                                                                                                                219
                                                                                                                                                                                                                                                                                                                           279
                                                                       159
                                                                                                                                                                       GGACTGGTCGCTCCCAGAAAGTCTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGC 309
                                                                                                                                                                                                                                                        248 GCCCAGCCCGTGGGGAAGGGAAAAGTGGGGATGGCTAAGAAAGCTGGGAAAATAGGG 189
                                                                                                                                                                                                                                                                                                                                                                                                          280 AACAGAAGAGGTAGTGGGTGGGCTAGGGGGCTGCCTTATTTAAAGTGGTTGTTTTATGA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAGAAGAGGTAGTGGGTGGGCTAGGGGCTGCCTTATTTAAAGTGGTTGTTTATGA 129
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2114172"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 551 Std Error: 0.00
Seg primer: -40UP from Gibco.
                                                                                                                              100 GGACTGGTCGGTGCCCAGAAAGTCTCTTCTGCCACTGACGCCCCCATCAGGGATTGGGCC
                                                                                                                                                                                                                       TTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCATGGCCTGCCATGACCTGCAGCCAA
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       Gaps
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    Indels
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                                           40 ATGCTGCTGCTAACGCTGCTGCTGCTGCTGCTG
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/lab_host="DH10B"
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Unpublished (1997)
  Conservative
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Matches 332;
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/clone_lib="NCI_CGAP_Kid11"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco R1; Plasmid DNA from the normalized library NCT_CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP prification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (5010nelDs 1322376-1323911, 1456007-1456775, and Fatima Bonaldo. "Butraction by Bento Soares and M. Patima Bonaldo."
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 517 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 CCTGCCTCATCGGCCTGCCATGACCTGCAAGCCCAAGCCCCGTGGGGAAGGGGAAGAA 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 GGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATA 106
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Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 TTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCTGTGTTCAATGTTTGTAAAGATT 46
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BEGAP), Tumor Gene Index Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                    62.3%; Score 291; DB 10; Length 406; larity 99.7%; Pred. No. 3.3e-134; Conservative 0; Mismatches 1; Indels
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3', mRNA sequence.
BF939932
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 ATATTAAGGCCCTGTTCATTAAGAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAG 48
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1 (basea 1 to 3010)
NCI/MTNDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Stsches and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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onaldo, Ph.D.
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                                  1. .612
/organism="Homo sapiens"
High quality sequence stop: 312.
Location/Qualifiers
                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:2432549"
                                                                    /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF939932.1 GI:12357252
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Homo sapiens
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                                    source
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                FEATURES
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Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, Ww., Hu, Ju.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungiun, Jr., Li, H., Meissner, P.S., Olsen, H., Baymond, L., Wei, Y.F., Ming, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Frassr, C.M., and Venter, J.C.

Frassr, C.M., and Venter, J.G.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI031859 409 bp mRNA linear EST 24-SEP-1998 oy45f12.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1668815 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                            For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MJ3 Reverse Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 GCTGCTTAAAGGCTCATGCTTGGAGTGGGACTGGTCGGTGCCCAGAAAGTCTCTTCTGC 131
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol type="mrNn"
/db_xref="ATCC (inhost):116104"
/db_xref="ATCC (inhost):116104"
/db_xref="warcon:0606"
/cell_type="endothelial cell"
/dev_stage="adult"
/clone_lib="Aorta endothelial cells, TNF alpha-treated"
/note="Gorgan: aorta; Vector: pBluescript SK-; Site_1:
BCORI; Site_2: Xhol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 TCATCGGCCTGCCATGACCTGCAAGCCCAAGCCCCGTGGGGGAAGGGGAAAGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 GCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCTCTTCTGC
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                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA 1821 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                               Other ESTs: THC174412
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI031859.1 GI:3250071
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Mammalia; Sutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 334)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Luee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hadblou, E., Hinkle, P.S.T.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.E., Saudek, D.M., Shrifey, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
                                                                                                                                                                                                                                                                               334 bp mRNA linear EST 18-APR-1997 EST17255 Aorta endothelial cells, TNF alpha-treated Homo sapiens CDNA 5' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 TACTAATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCTGT 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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  the I.M.A.G.E. Consortium/LLNL, send email
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                                                                                                                                                                                                      /clone="IMAGE:3439129"
/tissue type="glioblastoma (pooled)"
/lab_host="DH10B"
                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                 info@image.Ilnl.gov
Seg primer: -40UP from Gibco
High quality sequence stop: 292.
Location/Qualifiers
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AA101878 458 bp mRNA linear EST 11-MAY-1997 zk85f07.s1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:489637 3', mRNA sequence.
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I (Dases 1 to 396)
Hillier, L. Lemnon, G. Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hulkman, M., Kucaba, T., Lacy, M., Le, M., Le, M. Darso, B., Morris, M., Parson, P., Prange, C., Riffin, L., Rohlfing, T., Schallenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Travaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                       Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham.

_Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MC 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 396;
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/dev stage="umbilical vein, 1 passage"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.6%; Score 241; DB 9; Le
100.0%; Pred. No. 3.1e-109;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="GDB:3928326"
/db_xref="taxon:9606"
  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 241, Conservative
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                                                                                                                                                                                                                                     and Marra, M.
                      Homo sapiens
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AAO83737 GI:1625813
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 921 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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  1 (bases 1 to 409)
NCI/NINDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.8%; Score 242; DB 9;
100.0%; Pred. No. 1e-109;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1668815"
                                                                                  (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Suzuki, Y.,
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HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y. Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M. Nakamura, Y., Nagai, T., Sugano, S., Isogai, T.)

Unpublished (2000)

Contact: Takao Isogai
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Pred. No. 1e-107;
0; Mismatches 1; Indels
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
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/clone="PLACE1002140"
/tissue_trye="placenta"
/clone_lib="placenta"
/note="Vector: pME18SFL3"
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Homo sapiens
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1 (bases 1 to 458)
Hillier, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hulman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Soares pregnant uterus NbHPU"
/note="Organ: uterus; Vector: pT/T3-Pac; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I
                                                                                                                                                                                                                                                                                                                                            Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7e1: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 528 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham.
Location/Qualifiers
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'lab_host="DH10B"
                       GI:1645281
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                                                                  Homo sapiens (human)
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         Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 271)
Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C. Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library
Nat. Genet. 4, 373-380 (1993)
94004965
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                                                                                                                                                                                                                                                                                                                                                                                    Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ugarine_now_saptens
/mol_type="markha"
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/dev_stage="fetus"
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EcoRI; Site_2: EcoRI"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 GGCCTGCCATGACCTGCAGCCCAAGCCCAGCCCGTGGGGAAAGGGGGGAAAGTGGGGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 GGCCTGCCATGACCTGCAGCCCAAGCCCCGTGGGGAAAGGGGAAAAGTGGGGGATG
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                                                                                                                                                                                                                                                                                             The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
713: 3018699423
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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43.0%; Score 201; DB 9; L.
Best Local Similarity 99.6%; Pred. No. 2.9e-89;
Matches 251; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                            Other_ESTs: THC174412
Contact: Kerlavage, AR
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Homo sapiens
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1 (Dases 1 to 977)

2 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

1 (Inpublished (2001)

2 Contact: Genoscope Genoscope Genoscope Genoscope - Centre National de Sequencage

3 Pall-1906 EVRX cedex - France

3 Email: seqref@genoscope.cms.fr, Web: www.genoscope.cms.fr

4 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10757.r For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EOOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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AL570794 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI022YC23 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.genoscope.cns.fr/
gl-bin/cluster.cgi?seq=CS0D1022AB12NP1&cluster=10757.r. Contact
gl-bin/cluster.cgi?seq=CS0D1022AB12NP1&cluster=10757.r. Contact
Feng Liang Email : filang@alfetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1022AB12NP1.
Location/Qualifiers
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EST78761 Placenta I Homo sapiens cDNA, mRNA sequence.
AA367347
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Pred. No. 3.5e-91;
0; Mismatches 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI022YC23"
                                                                   AL570794.2 GI:31292209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 GTGGGTGGCTAGGGG 138
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Best Local Similarity 99.6%;
Matches 255; Conservative
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AA367347/c
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JOURNAL
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                                        ACCESSION
VERSION
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ALS71908 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA Clone CSOD1029YL01 3-PRIME, mRNA sequence.
ALS71908
ALS71908
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 ACTAATITATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTG 406
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1880
Fax: 314 286 1880
Fax: 314 286 1880
Fax: 314 286 1880
High quality sequence stops: 355
Source: IMAGE Consortium, LANL
This clone is available royaluy-free through LANL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 GAGGGIAGTGGGCTAGGGGGCCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 GAGGGTAGTGGGCTAGGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGANTCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 ACTAATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCTGTG
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                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRKA"
/dol_xref="GDB:41555"
/db_xref="taxon:9606"
/clone="IMAGB:43014"
                                                                                                                                                                                                                                                                                                High quality sequence stop: 363
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'sex="female"
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Homo sapiens
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AL571908/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; Normalized infant brain cDNA library made by Dr. M. Soares (Columbia University), oligo-dr primed and directionally cloned between HindIII (5') and NotI (3') sites "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 CTGTGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCCAGCCCCGTGGGGAA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 GOCCAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGGTAGTGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 GTGGGCTAGGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATA 357
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                   Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032706637
Eax: 3032707097
Email: nikki@tally.uchsc.edu
Seq primer: -21M13 Universal.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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/clone="LiAB311B03"
/clone_lib="Infant brain,
1NIB"
                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                     Human cDNAs from infant brain
Unpublished (1993)
Contact: Sikela JM
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Matches 255; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BMail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10757.r For
                                                                                                                                                                                http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI029CF01NPl&cluster=10757.r. Contact
cgi-bin/cluster.cgi?seq=CSODI029CF01NPl&cluster=10757.r. Contact
cgi-bin/cluster.cgi?seq=CSODI029CF01NPl.:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI029CF01NPl.
Location/Qualifiers
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 1201)
Mannalia, Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10757.r For
more information about this cluster, see
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cgi-bin/cluster.cgi?seq=cSoDi012BE05NP1&cluster=10757.r. Contact
Feng Liang Email : fliang@lifete.ch.com VRL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI012BE05NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 CCCTGTTCATTAAGAAATTGTTCCCTTCCCTGTGTTCAATGTTTGTAAAGATTGTTCTG
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Feb 16, 2001 this sequence version replaced gi:12929669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.4%; Score 156; DB 9; Length 1200; 100.0%; Pred. No. 1.1e-66; ive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                    organism≈"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                         clone="CS0DI029YL01"
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Contact: Genoscope
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BF589966 229 bp mRNA linear EST 12-DEC-2000 naa33h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258458
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                              /LISSUE TYPE="PLACENTA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized."
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NCI-(CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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info@image.llnl.gov
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                                                                                                                                      'organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:3258458"
                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                      /clone="CS0DI012YI10"
Location/Qualifiers
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Location/Qualifiers
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Query Match
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/lab_lab_lab_lab_lab.
//clone_lib="Nature" (App. Kidl1"
//clone_lib="Nature" (App. Kidl1"
//clone_lab="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Ecc RI;
Plasmid DNA from the normalized library NoT CGAP Kid3 was prepared; and ss circles were made in vitro. Rollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pol of 5,000 clones made from the same library (clonelDs 13223%-1323911, 1456007-1456775, and 150052-1502855). Subtraction by Bento Soares and M.
                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX118770 52 Etal heart NDHH19W Homo sapiens cDNA clone IMAGD998G06783 ; IMAGE:342941, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                               285 AAGAGGGTAGGGCTAGGGGGGGCCTGCCTTATTAAAGTGGTTGTTTATGATTCTT 344
                                                                                                                                                                                                                                                                                                                                                                                                                  345 ATACTAATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCTG 404
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I (bases 1 to 528)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Umpublished (2003)

Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free from RZPD; contact RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 ATACTAATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 IGTICAAIGITIGIAAAGAITGTICIGIGIAAAIAIGICITITAIAAAAAGGITAAAAG
                                                                                                                                                                                                                                                                                                  Gaps
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                           28.3%; Score 132; DB 10; Length 229; 99.5%; Pred. No. 8.7e-55;
                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BX118770.1 GI:27882396
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Matches 182; Conservative
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ORGANISM
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AUTHORS
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JOURNAL
COMMENT
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LOCUS
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KEYWORDS
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W67823 Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone IMAGE:342941 5', mRNA sequence.
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Mamalla, Eutheria, Primates; Catarrhini, Hominidae, Homo.
1 (Dases 1 to 596)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Rucaba,T., Le,M., Lenno,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TCTTATAGTAATTTATAGAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL , contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 630 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                           27.2%; Score 127; DB 13; Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
clone="IMAGp998G06783 ; IMAGE:342941"
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                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. ...
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/organism="Homo sapiens"
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/db_xref="GDB:1268316"
/db_xref="taxon:9606"
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High quality sequence stop: 394
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
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Matches 127; Conservat
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Email: cgapbs-remail.nih.gov
Tissue Prourement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 468.
Location/Qualifiers
                                                                                                                                      brilaby4 hr72a04.xl NCI_CGAP_Kidil Homo sapiens cDNA clone IMAGE:3133998 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AATITATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCTGTGTTC 60
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 544)
                                                                                                                                                                                                                                                                                                                                                    double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAACAGTTAAAAGCTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 AATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTC
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="GDB:1323684"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:3133998"
                                                                   /db_xref="taxon:9606"
/clone="IMAGE:415214"
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                                                                                                                    /sex="male"
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Matches 118; Conservative
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BF114974/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CCTGTGTTCAATGTTTGTAAGATTGTTCTGTGTAAATATGTCTTTATAATAATAAAAAGTTA 120
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Hillier, L. Lemnon, G. Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Haukins, M., Rucaba, T., Lacy, M., Le, M., Le, M., Le, M. Mardis, E., Moore, B., Morris, M., Parsons, J., Parange, C., Rikin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                          normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 720 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TCTTATACTAATTTATACAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCC
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.2%; Score 127; DB 14; Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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High quality sequence stop: 451.
Location/Qualifiers
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                                                 stage="19 weeks"
    clone="IMAGE:342941"
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314 286 1810
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SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

ACCESSION

VERSION KEYWORDS

RESULT 32

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W91937

source

FEATURES

MEDLINE PUBMED COMMENT

TITLE JOURNAL

0 409

Query Match

Best Local

Matches

Indels

80; Conservative

Matches

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a modified polylinker; Site 1: Not I; Site 2: Eco RI; basmid DNA from the normalized library NoT CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and Fatima Bonaldo. "Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Peripheral Nervous system"
/lab_host="DH108 (T1 phage-resistant)"
/clone_lib="Human Anterior Horn"
/note="Vector: pCMV-SPORT6.1; Site_1: EcoRV (destroyed);
Site_2: Not1; Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 2.1 kb. Library was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF456943 885 bp mRNA linear EST 04-SEP-2003
AGENCOURT 15337517 Human Anterior Horn Homo sapiens cDNA clone
IMAGE:305I4432 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                       446
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 885)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAMS77 row. o column: 17

High quality sequence start: 4

High quality sequence store: 4

High quality sequence store: 598.

Location/Qualifiers

1.885

/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                  387 AATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATAIGTCTTT
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHE-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                           Length 544;
                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                        17.3%; Score 81; DB 10;
100.0%; Pred. No. 3e-29;
ative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics NIH National Cancer Institute / NIH Bldg. 31 Rml0A07 Bethesda, MD 20892 Bmail: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30514432"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 ATAATAAACAGTTAAAAGCTG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 ATAATAACAGTTAAAAGCTG 464
                                                                                                                                                                                                             Fatima Bonaldo
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Length 885;

DB 14; 1e-28;

17.1%; Score 80; 100.0%; Pred. No.

Query Match Best Local Similarity

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                                                                        624 CAATGITIGCCIAICCACCICCCCCAAGCCCCTTTACCTAIGCIGCIAACGCTGCTGC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                zn39d09.rl Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:549809 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -28M13 rev2 from Amersham
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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0
0; Mismatches
                                    1 CAATGITIGCCTATCCACCTCCCCAAGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRRA"
/db_xrefe="GDB:3928326"
/db_xrefe="taxon:9606"
/clone="IMAGE:549809"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 324
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                                                                                                                                      684 CTGCTGCTGCTGCTTAA 703
                                                                                                            61 CIGCIGCIGCIGCITAA 80
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seq29-na-truncated.olig10.rst

21

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

RESULT 36 AI871137/c DEFINITION

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/clone="INMAGE:586800"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Metastatic Chondrosarcoma"
/dev_stage="Metastatic Chondrosarcoma"
/dev_stage="Metastatic Chondrosarcoma"
/lab_host="DH10B (Life Technologies)"
/locte="Organ: Lung; Vector: pT713-pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP DT0 is a cDNA library containing the following tissue (s): Metastatic Chondrosarcoma in Lung; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oilgo-dry primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into pT713-pac vector: The oilgonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I is the and the
                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov POLYA=yes.
                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 556)
NCI-CAR http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 640)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      537 AATGITIGTAAAGAITGITCIGIGIPAATAIGICITIATAATAAAACAGITAAAAGGCIG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 AATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAAAGAGTTAAAAAGCTG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM992527
UI-H-DT0-att-k-01-0-UI.s1 NCI_CGAP_DT0 Homo sapiens cDNA clone
IMAGE:5864184 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAG_TISSUE=lung metatastic chondrosarcoma
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9.3e-18;
                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
12.4%; Score 58; DB
Best Local Similarity 100.0%; Pred. No. 9.3
Matches 58; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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TAG_SEQ=AACTGTTCGG"
                                    BM994192.1 GI:19719093
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                                                                                           Homo sapiens (human)
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Homo sapiens
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .556
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BM992527/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

Unsert Length: 669 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 455.

1.:557
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UI-H-DT0-atx-n-09-0-UI.s1 NCI CGAP_DT0 Homo sapiens cDNA clone
IMAGE:5865800 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 557)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2431144"
                                                                                                                                                                                                                                       AI871137.1 GI:5545105
207 GCCCAGCCCGTGGG 221
                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                             sapiens
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EST 17-JUN-2002

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RESULT 37

Query Match

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Best Loc Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Lissue_type="Myatariatic Chondrosarcoma"
/dev stage="Madult"
/lab_host="Adult"
/lab_host="DHIOB (Life Technologies)"
/clone_lib="NoT (GAP DTO"
/note="Organ: Lung, Vector: pT7T3-pec (Pharmacia) with a modified polylinker; Site_l: BCOR I; Site_2: Not I;
NCI_CGAP DTO is a cDNA library containing the following visue(s): Metatastic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligomaclectide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)B tail. The sequence tag for this library is
                                                                                                                             Email: cgapbs-r@mail.nib.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M. M.G.B. Consortium/LMML at: http://image.llnl.gov
Through the I.M. M.G.B. Consortium/LMML at: http://image.llnl.gov
sequence: 1-21, >AT zich#Low_complexity (matched compliment)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dasea 1 to 744)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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TAG_LIB=UI-H-DT0
TAG_SEQ=AACTGTTCGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGE:5864184"
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BQ006379.1 GI:19731279
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BQ006379/c
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     AUTHORS
TITLE
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TITLE
                                                                                    JOURNAL
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/clome_lib="NCI_CGAP_EII"
//note="Organ: Left Pelvis; Vector: pI7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574 bp mRNA linear EST 03-MAY-2002
hd52b09.g1 Canis Total Brain cDNAs Canis familiaris cDNA clone
hd52b09 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dI)18 tail. The sequence tag for this library is
           CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov The following repetitive elements were found in this cDNA Sequence: 1-21, >AT rich#Low_complexity (matched compliment) POLYA=Yes.
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 574)
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Bahret, A., Cunnius, D., Dedhia, N.N., de la Bastide, M.,
Kazenberger, F., King, L., Kirchoff, K.A., Miller, B., Muller, S.,
Kazenberger, F., King, L., Kirchoff, K.S., Spiegel, L.A.,
Zutavern, T., Santos, L. and Hannon, G.J.
Expressed sequence tags from Canis familiaris (dog) (5_2002)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Hazbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
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11.1%; Score 52; DB 12; Length 744;
Best Local Similarity 100.0%; Pred. No. 9.6e-15;
Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="Chondrosarcoma"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
lissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_IISSUE=chondrosarcoma
TAG_LIB=UI-H-EI1
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5846098"
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Canis familiaris (dog)
Canis familiaris
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once through E. coli XL1-Blue MRF'."
                                                             Query Match
Best Local Similarity 100.0%; Pr
Conservative 0;
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Direct Submission
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/note="Westor: Lambda ZAPII; Site 1: EcoRI; Site 2: XhoI;
Second generation merozoites of E. tenellaH were purified
by column chromatography and mRNA extracted using a
FASTTRACK kit (Invitrogen). cDNA was synthesised and a
Uni-ZAP XR library was constructed using cDNA synthesis
kit, ZAP-CDNA synthesis kit and ZAP-CDNA Gigapack III
Gold cloning kit (Stratagene). The library was amplified
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                                                                                                                                                                                                /clone_lib="Camis Total Brain cDNAs"
/clone_lib="Vector: Lambda Zap II; The library was provided by Greg Hannon and Lee Santos (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using stratagene zap CDNA synthesis kit. It was made from dog whole brain cells. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Wan,K.L., Chong,S.P., Ng,S.T., Tomley,F.M. and Jangi,M.S.
Survey of genes in Eimeria tenella merozoite
Unpublished (1999)
Contact: Wan KL
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                                                                                                                                                                                                                                                                                                                                                                              Length 574;
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Clone="etm\055"
dev stage="second generation merozoite"
/lab_host="XL1-Blue MRF""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              395 TATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 TATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCT 375
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Local Similarity 100.0%; Pred. No. 2.9e-09;
nes 41; Conservative 0; Mismatches 0;
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Universiti Kebangsaan Malaysia
43600 UXM Bangi, Selangor DE, Malaysia
8251997
Fax: 6 03 8293949
Email: Klwan@pkrisc.cc.ukm.my
                                                                                                          1. .574
/organism="Canis familiaris"
/mol_type="mRnA"
/db_xref="taxon:9615"
/clone="hd52b09"
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             Email: mccombie@cshl.org

Plate: hd52 row: b column: 09
Seq primer: -21Ml3UnivRev

High quality sequence stop: 574.
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/strain="Houghton"
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A1676745.1 GI:4877225
EST.
Fax: 516 367 8874
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Eimeria tenella
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BACKWARD: T7
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AI676745/c
LOCUS
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ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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CNSO5DCI 972 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T3 end of clone 042N02 of library A from Tetraodon nigroviridis, genomic survey
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
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Estimate of human gene number provided by genome-wide analysis
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/organism="Tetraodon nigroviridis"

/mol_type="genomic DNA"

/mol_type="genomic DNA"

/clone="042NO2"

/clone lib="A"

/note="Genoscope sequence ID : COAAO42DGO1A1~end : T3"
                                                                    Gaps
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   Length 491;
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Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                               486 TGCTGCTAACGCTGCTGCTGCTGCTGCTGCTGCT 453
Score 34; DB 9;
Pred. No. 9e-06;
0; Mismatches (
                                                                                                                        44 TGCTGCTAACGCTGCTGCTGCTGCTGCTGCT 77
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6.4%; Score 30; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 30; Conservative 0; Mismatches
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GSS; genome survey sequence.
Tetracdon nigroviridis
Tetracdon nigroviridis
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/organism="Homo sapiens"

/mol type="WRIX"

/db_xrefe"taxon:9606"

/dlone="f66500"

/clone="Toecor: pSPORTI; Site_1: Mlul; Site_2: Notl; mRNA

/note="Toecor: pSPORTI; Site_1: Mlul; Site_2: Notl; mRNA

was prepared from human testis of a 27 years old man. cDNA

was prepared from human testis of a 27 years old man. cDNA

was prepared using a 15mer oligo dT anchored by two

degenerated bases at its 3'end and containing a Notl site

at its 5'end. The CDNA was cloned between Sall and Notl

sites of pSPORTI. The Mlul-Sall fragement come from the

adaptator used for the cloning. The 3' end is at the Notl

site. cDNA corresponding to abundant species were

eliminated from this library."
                                                                                                                                                                                                                                                                                                                                                                                                           Unite INSERM 99, Hopital Henri Mondor, 94010 Creteil, France Tel: (33)149813530
Fax: (33)148980908
Email: guellaen@infobiogen.fr
This sequence derives from a clone which was selected from the cDNA library - Testis 5 - using a repeat of 14 CAG as probe
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                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 405)
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Leishmania braziliensis GSS, clone LBAF096B01, genomic survey
  f06500r Testis 5 Homo sapiens cDNA clone f06500 3' end, mRNA
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Leishmania, Leishmania braziliensis species complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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100.0%; Pred. No. 0.0028;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                   Guellaen, G. Unpublished (1996)
Unpublished (1996)
Contact: Guellaen G
Unite INSERM 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX541495
BX541495.1 GI:32139660
GSS; genomic survey sequence.
Leishmania braziliensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seg primer: M13 reverse.
Location/Qualifiers
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                                                                               GI:1929211
                                                                                                                                Homo sapiens (human)
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Best Local Similarity 100.0
Matches 29, Conservative
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                                                                                                                                                           Homo sapiens
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AA065331.1
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                             sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                INSERM
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LBAF096B01
DEFINITION
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                                                                                                                                                                                                                                                                             Eukaryota, metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Bukaryota, metazoa, Chordata, Craniata, Vertebrata; Butheria; Butheria; Bruharia; Butheria; Bruharia; Bruharia; Butheria; Bruharia; Bruharia; Bult, C.J., Lee, N.R., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gooayne, J.D., Mile, C.J., Lee, N. Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Ghelm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.T., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Peng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wal, Y.S., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Pisser, C.M. and Veneer, J.C.
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                                                                               EST 21-APR-1997
                                                                         AA363384

SST 21-APR-1997

EST73237 Ovary I Homo sapiens cDNA 5' end similar to similar to H.
sapiens hypothetical protein CTG-B33 (GB:L10376), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org

Email: arkerlav@tigr.org

For clone and expression

information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult, 71 yrs"
/clone_lib="Owary 1"
/note="Organ: ovary, Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: Xho!"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
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/mol_type="mRNA"
/db_rare="AATCC (inhost):167640"
/db_rare="taxon:9606"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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                                                                                                                                                                                   AA363384.1 GI:2015704
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Contact: Kerlavage, AR
                                                                                                                                                                                                                                    Homo sapiens (human)
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                        RESULT 43
AA363384
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6.2%; Score 29; DB 14; Length 482; 00.04; Pred. No. 0.0028; ve 0; Mismatches 0; Indels
                                    1 Similarity 100.0%; Fred. No. 0.0 29; Conservative 0; Mismatches
                                                                                                                  182 GCTGCTGCTGCTGCTGCTGCTTAAAG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 GCTGCTGCTGCTGCTGCTTTTAAAG 501
                                                                                           54 GCTGCTGCTGCTGCTGCTGCTTAAAG 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                             BG328052.1 GI:13134490
                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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                                                                                                                                                                                                                                                           mRNA sequence.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High qality sequence stops: 224 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 613 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 224.
                                                                                                                                                                                                                                                                                                                                                 482 bp mRNA linear EST 09-FEB-1995 yb60h09.rl Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:75617 5', mRNA sequence.
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Bukaryota.

Bukaryota.

Mammalia. Eutheria.

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Mammalia. Eutheria.

Mammalia.

Millier,L.

Mariono,G.

Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,

Mardis,E., Moore,B., Worris,M., Parsons,J., Prange,C., Rifkin,L.,

Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,

Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,

Travaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                Length 423;
                                                                                                                                                                                                  0; Indels
                    1. .423
/organism="Leishmania braziliensis"
/mol_type="genomic DNA"
/srrain="WAOM/BR/75/M2904"
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                                                                                                                                                              Score 29; DB 29;
Pred. No. 0.0028;
                                                                                                                                                            th 6.2%; Score 29; DB Similarity 100.0%; Pred. No. 0.0 29; Conservative 0; Mismatches
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/db_xref="GDB:505346"
/db_xref="taxon:9606"
/clone="IMAGE:75617"
ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                      T58423.1 GI:660260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
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KEYWORDS
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FEATURES
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COMMENT

ORIGIN

T58423

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ORIGIN

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/d.zee_TiMAGE:457111"

/tissue type="adenocarcinoma cell line"
/lab.host="BH10B (phage-resistant)"
/clone lib="NHH WC 15"
/clone line box1/Xhol sites using the following 5/
adaptor: GGCACGAG(G). Site=selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald W. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis Kit
(Stratagene) and Superscript II RT (Life Technologies)"
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BG528108
BG528108.1 GI:13519645
EST.
                                                                                                                                                                                                                                                                                                                   BG328052 732 bp mRNA linear EST 27-FEB-2001
602427694F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4547111 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 732)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Flate: LLCML234 row: 1 column: 24
High quality sequence stop: 630.
   Gaps
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100.0%; Pred. No. 0.003;
tive 0; Mismatches 0; Indels
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Contact: Tadasus snnn.1
Center For Genetic State Martin Shizuoka 411-8540, Japan
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Fax: 81-559-81-6855
Email: Ishinidgenes.nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phage vector (Carninci et al. 2001). 5, end of the CDNA that was digested with XhoI was ligated to Sall site of the vector and the 3' end including polyA tail was ligated to BamHi site of the vector and the 3' end including polyA tail was vector(5'- gAgAgAgArCCAACCCTggAgAgTTTTTTTTTTTTTTTVN-3' was used as a lst 3' primer, and
5'-ggTTCTCgAGATCGACACAGAGACAGCGATGACGCONNNN-3' as 2nd 5'-ggTTCTCgAGTCTTCGAGAACGCGATGCGCACACGAACAGCGATGCGCGAGATGCGCGAGTCGAATTCGTCGAGAACGCGATGCGAATCGGCGGATCGAATTCGTCGAGAACGCGATGCGAATCGGCGGTCTGAATTCGTCGAGAACGCGAATGGCGAGTCGAATTCGTCGAGAACGCGAATGGCGAGTCGAATTCGTCGAGAACGCGAATGGCGAGTCGAATTCGTCGAGAACGCGAATGGCGAGTCGAATTCGTCGAGAACGCGAATGGCGAGTCGAATTCGTCGAGAACGGCAGAACGGCAGTCGAATTCGTCGAGAACGGCAATGGCGAGTCGAATTCGTCGAGAACGGAATGGCGAATGGCGAGATGGAATTCGTCGAGAACGGCAGAACGGAATCGGCGAGATGGAATTCGTCGAGAACGGAATGGCGAGATGGAATTCGTCGAGAACGGAATGGCAGAATTCGTCGAGAACGGAGATGGAATTCGTCGAGAACGGAATGGCAGAATTCGTCGAGAACGGAATGGCGAGATGGAATTCGTCGAGAACGGAATGGCAGAATTCGTCGAGAACGGAATGGAATGGCAGAATTCGTCGAGAACGGAATGGAATGGAATGGAATTCGTCGAGAAGAGGAATGGAATGGAATGGAATGGAATTCGTCGAGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATTCGTCGAGAATGGAATGGAATGGAATGGAATGGAATGGAATTCGAGAAAGGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATTCGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA
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345 bp mRNA linear EST 03-MAR-20
ga66a05.y1 Moss EST library PUV Physconitrella patens cDNA clone
PEP SOURCE ID:PPUI.0509 5' similar to TR:Q9ZVB7 Q9ZVB7 PUTATIVE
STRICTOSIDINE SYNTHASE. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="mixture of chloronemata, caulonemata and rhizoid-like protonemata" /clone_lib="normalized full length cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Physcomitzella patens
Physcomitzella patens
Eukaryota patens
Bukaryota patens
Eukaryota patens
Eukaryota patens
Eukaryota patens
Eropeida, Funariales, Funariaceae, Physcomitzella.
I (bases 1 to 345)
Quatrano, R., Bashiardes, S., Cove, D., Cuming, A., Knight, C., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B., Jackson, Y., McCann, R., Waterston, R., Waterston, R., Waterston, R., Waterston, R., Markon, M., Milson, R., Harvey, N., Ritter, E., Jackson, Y., Moss EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Physcomitrella patens subsp. patens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%; Score 28; DB 12; Length 323;
100.0%; Pred. No. 0.0085;
iive 0; Mismatches 0; Indels
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Leeds/Wash U Moss EST Project
Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="pphn28014"
                                           Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW509816.1 GI:7147894
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Best Local Similarity
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AW509816
LOCUS
DEFINITION
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                                        COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_tropolitoreogidermoid carcinoma"
/lab_host="NDH_MGC_59"
/clone_lib="NIH_MGC_59"
/clone_lib="NIH_MGC_59"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattacggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCCATTATGGCC_3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGGCATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: capbs-rammali.nih.gov

Tissue Procurement: Arco.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://mage.llnl.gov. o column: 21
High quality sequence stop: 594.
Location/Qualifiers
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BJ600203 GI:37842195
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22709184
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Pred. No. 0.0031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4686572"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 GCTGCTGCTGCTGCTGCTTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
Homo sapiens (human)
                                 Homo sapiens
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EST 03-MAR-2000

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Tell 314 266 1800

Fax: 14 266
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Query Match
6.0%; Score 28; DB 10; Length 345;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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g

Search completed: May 25, 2004, 19:19:03 Job time : 2889 secs

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Sequence 1, Appli
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Sequence 7, Appli
Sequence 75, Appli
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Sequence 16656, Appli
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1, Appli
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Sequence 14, Appl
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                                                                           May 25, 2004, 15:14:46; Search time 95 Seconds (without alignments) 2728.022 Million cell updates/sec
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-232-463-14
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US-08-468-853-7
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US-08-468-853-7
US-08-205-995-75
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US-08-457-273B-41
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                                                                                                                                                                                                                         682709 segs, 277475446 residues
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                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                SEQ29-NA-TRUNCATED
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:

Suite 500

CORRESPONDENCE ADDRESS: ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, CITY: Alexandria

COUNTRY: USA ZIP: 22313-0299

NUMBER OF SEQUENCES:

29,768 ER: 30472/114 IMMU

TELECOMMUNICATION INFORMATION

TELEPHONE: (703)836-9300 TELEFAX: (703)683-4109 REFERENCE/DOCKET NUMBER:

TELEX: 899149 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

7218 base pairs

FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNAY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313

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1339
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100.0%; Score 467; DB 4; Length 50000;
Best Local Similarity 100.0%; Pred. No. 1.5e-136;
Matches 467; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                APPLICANT: Ryan, James W.
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Sprinkle, Terry Joe Curtis
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
GURRENT FILING DATE: 1998-09-02
BARLIER APPLICATION NUMBER: 60/057,854
BARLIER PILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
ALIGNMENTS
                                                                                                                                             Sequence 4, Application US/09146053A Patent No. 6399349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                        RESULT 1
US-09-146-053-4/c
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66 GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCTC 125
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                                                                                                                       h 8.7%; Score 40.4; DB 1; Length 7218; Similarity 2.3%; Pred. No. 0.034; 5; Conservative 134; Mismatches 75; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                       186 CCTGCCTCATCGGCCTGCCATGACCTGCAGCCAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-521-511C-10/c
Sequence 10, Application US/09521511C
Patent No. 6555358
GENERAL INFORMATION:
APPLICANT: Gurnett, Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schmatz, Dennis
APPLICANT: Harris, Georgianna
APPLICANT: Rattray, Sandra J.
TITLE OF INVENTION: CYCLIC GMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liberator, Paul A.
Donald, Robert
TYPE: nucleic acid
STRANDEDNESS: single
                                                                   ; CLONE: pTZgpt-F1s
US-08-232-463-14
                                   linear
                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                IMMEDIATE SOURCE
                                   TOPOLOGY:
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APPLICANT:
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Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHETFLINGER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

US-08-232-463-14

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408 riecriecrierracriecriecriecriecriecriecriecricarcecceaakasariecacagaes 349
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                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Chandy, George K.
APPLICANT: Chandy, Jay J.
APPLICANT: Gargue, Jay J.
APPLICANT: Gargue, Jay J.
APPLICANT: Gargue, Jay J.
APPLICANT: Gargue, Emmanuelle
APPLICANT: Kalman, Katarin
TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
TITLE OF INVENTION: MARKER AND THERAPEUTIC TARGET
TITLE OF INVENTION: MARKER AND THERAPEUTIC TARGET
TITLE OF INVENTION: MARKER AND THERAPEUTIC TARGET
TITLE OF INVENTION: 103106/01401
FILE REFERENCE: 07306/01401
CURRENT PILLING DATE: 2990-01-04
PRIOR FILING DATE: 1998-01-04
PRIOR FILING DATE: 1998-01-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2521
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APPLICANT: Chandy, George K.
APPLICANT: Gargus, Jay J.
APPLICANT: Gargus, Jay J.
APPLICANT: Gargus, George
APPLICANT: Gargus, George
APPLICANT: Fantino, Emmanuelle
APPLICANT: Ralman, Katarin
TITLE OF INVENTION: MCCA3/KCNN3 SMALL CONDUCTANCE CALCIUM
TITLE OF INVENTION: MCCA3/KCNN3 SMALL CONDUCTANCE A DIAGNOSTIC
TITLE OF INVENTION: MARKER AND THERAPEUTIC TARGET
TITLE OF INVENTION: MARKER AND THERAPEUTIC TARGET
TITLE OF INVENTION: MARKER AND THERAPEUTIC TARGET
TITLE REPRICATION NUMBER: US/09/115,446
CURRENT FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/052,556
EARLIER RILING DATE: 1998-01-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2526
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Pred. No. 0.21;
0; Mismatches
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                                                        Sequence 1, Application US/09565590 Patent No. 6653100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.9%;
Best Local Similarity 64.7%;
Matches 55; Conservative C
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; LOCATION: (287)...(2479)
US-09-565-590-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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                    US-09-565-590-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 TIACCIAIGETGCIGCIAAAGGCIGCIGCIGCIGCIGCIGCIIAAAGGCICAIGCIIG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
CHEMOTHERAPEUTIC TARGET FOR ANTIPROTOZOAL AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chandy, George K.
APPLICANT: Chandy, Jay J.
APPLICANT: Garque, Jay J.
APPLICANT: Garque, Jay J.
APPLICANT: Garque, Jay J.
APPLICANT: Fantino, Emmanuelle
APPLICANT: Fantino, Emmanuelle
APPLICANT: Kalman, Katarin
TITLE OF INVENTION: ACCAS, KCNAS SMALL CONDUCTANCE CALCIUM
TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
TITLE OF INVENTION: ARKER AND THERAPEUTIC TARGET
TITLE OF INVENTION: MARKER AND THERAPEUTIC TARGET
FILE REPERENCE: 07306/014001
CURRENT APPLICATION NUMBER: 06/09/115,446
CURRENT PILING DATE: 1998-07-14
EARLIER RILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-01-08
NUMBER OF SEQ ID NOS: 15
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 8.2%; Score 38.2; DB 4; Length 4262; 1 Similarity 59.8%; Pred. No. 0.12; 64; Conservative 0; Mismatches 43; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 Gagracacarcacardeccanananarcrarrargacacacaga 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 TTĠŦĠĠĠĊĠĠĊŖĠĊŦŖĠŖĠŖĠŖŖĠĠĠĠĠĠĸĠĊŖĠĸĊŦĠŔĠĠ 307
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          FILE OF INVENTION: CHEMOTHERAPEUTIC TARGET IS FILE REFERENCE: 2036 CURRENT APPLICATION NUMBER: US/09/521,511C CURRENT FILING DATE: 2000-03-08 PRIOR APPLICATION NUMBER: 60/129,058 PRIOR FILING DATE: 1999-04-13 NUMBER OF SEQ ID NOS: 16 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10 SE
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Patent No. 6165719
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Best Local Similarity 64.7*
warrhes 55; Conservative
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LOCATION: (287)...(2479)
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US-09-521-511C-10
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Best Local Similarity
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van den BOOGAART, Paul
KOK, Jacobus Johannus
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US-09-539-333D-178
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Patent No. 5670362
GENERAL INFORMATION:
APPLICANT: Van den BOGGAART, Par
APPLICANT: KOK, Jacobus Johannus
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LOCATION: 1489...1513
OTHER INFORMATION: 99-15682-318
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Matches 88; Conservative
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ORGANISM: Homo Sapiens
FEATURE:
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LOCATION: 1842
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APPLICANT: Cohen, Daniel
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenfeld, Marta
APPLICANT: Bihain, Bernard
APPLICANT: Chumen associated Genes, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: GENSET. 047AUS
CURRENT APPLICANTION NUMBER: US 60/126,903
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR APPLICATION NUMBER: US 60/132,065
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                                                                                 41 TGCTGCTGCTACGCTGCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGG 100
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                                                                                                                                   413 TGCTGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTCTCTCCCAGAGGATGGACAGGGG 354
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                                0; Gaps
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TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
TITLE OF INVENTION: ARKER AND THERAPEUTIC TARGET
FILE REFERENCE: 07306/01401
CURRENT APPLICATION NUMBER: US/09/565,590
CURRENT APPLICATION NUMBER: 08/09/565,590
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-01-08
NUMBER OF EQ ID NOS: 15
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Best Local Similarity 64.7%; Pred. No. 0.21;
Matches 55; Conservative 0; Mismatches 30; Indels
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FastSEQ for Windows Version 4.0
                                                                                                                                                                                       101 GACTGGTCGGTGCCCAGAAGTCTC 125
                                                                                                                                                                                                                                                  353 CACTTGGGGTCTTCATCCAAGTCCC 329
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GENERAL INFORMATION:
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Patent No. 6653100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gargus, Jay J.
APPLICANT: Gurdan, George
APPLICANT: Fantino, Emmanuelle
APPLICANT: Kalman, Katarin
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Gargus, Jay J.
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US-09-565-590-5
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SEQ ID NO 5
LENGTH: 2526
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2014 AAGAAATAAAGACATGAAAAGTGGCAAGACTTAATCTGATCTCTGTGTATGTGATGCTT 2073
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LOCATION: 1665..1683
OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3001;
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LOCATION: 1501
OTHER INFORMATION: 99-15682-318 : polymorphic base A or T
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50.6%; Pred. No. 0.36;
tive 0; Mismatches 86;
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NAME/KEY: primer bind
LOCATION: 1184..1202
OTHER:
FEATURE:
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/143,928
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR FILING DATE: 1999-07-29
PRIOR PILING DATE: 1999-07-29
PRIOR PILING DATE: 1999-07-29
PRIOR PILING DATE: 1999-10-28
PRIOR PELING DATE: 1999-10-28
PRIOR PELING DATE: 1999-10-28
PRIOR PELING DATE: 1999-10-18
PRIOR PELING DATE: 1999-10-18
PRIOR PELING DATE: 1999-10-12
PRIOR PELING DATE: 1999-10-12
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NOAME/KEX: misc_binding
LOCATION: 1502.1521
OTHER INFORMATION: 99-15682-318.mis2,
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NAME/KEY: misc binding
NAME/KEY:
OTHER INFORMATION: 99-15682-318.misl
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                                                             5780289el Patent Department
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION NATHER: US/08/468,855
FILING DATE: 06-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 77, Application US/08310357; Patent No. 5789233; GENERAL INFORMATION:
APPLICANT: van den BOOGAART, Paul
APPLICANT: VOK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
7.7%; Score 35.8; DB 1;
Best Local Similarity 63.2%; Pred. No. 0.24;
Matches 55; Conservative 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 06-UTN-1995
CLASSIPRICATION: 435
PRICA APPLICATION DATA:
APPLICATION WUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRICA APPLICATION DATA:
APPLICATION WUMBER: US 08/102,865
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-UTN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-UTN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-UTN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MATY E. GOTTLEY
REGIETATION NUMBER: 34,409
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 800 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
          NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ARZO NO. 5780286
STREET: 1300 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
                                                                                    STATE: Marville
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                                                                                                                                                         U.S.A.
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CLONE: EAM20E
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; LOCATION: 2...E
US-08-468-855-7
                                                                                                                                                         COUNTRY: U
ZIP: 20850
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APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCR ADDRESS:
ADDRESSE: Akro No. 5670362el Patent Department
STREET: 1300 Piccard Drive
CITY: Rockville
CITY: Rockville
CITY: D45050
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US 08/310,357
FILNG DATE: 21-SEP-1994
FILNG DATE: 06-AUG-1993
FILNG DATE: 06-AUG-1993
FILNG DATE: 18-JUN-1992
FILNG DATE: 18-JUN-1992
FILNG DATE: 18-JUN-1992
FILNG DATE: 18-JUN-1992
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US-08-468-855-7/c
; Sequence 7, Application US/08468855
; Parent No. 5780289
; GENERAL INFORMATION:
; APPLICANT: van den BOGGAART, Paul
APPLICANT: KGK, Jacobus Johannus
; APPLICANT: VERMEULEN, Arnoldus Nicolaas
; TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TORNEY/AGGINAL NAME: Mary E. Gormley
NAME: Mary E. Gormley
34,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,409
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA to mRNA
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Matches 55; Conservative
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MOLECULE TYPE: CDN
IMMEDIATE SOURCE:
CLONE: Eam20E
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; LOCATION: 2...
US-08-468-853-7
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Gaps

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TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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Best Local Similarity 63.22
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double
                                                                                                                                                                                          FILING DATE: 06 CLASSIFICATION:
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CLONE: Eam20E
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STRANDEDNESS:
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US-08-468-857-7/c
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US-08-468-852-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.7%; Score 35.8; DB 1; Length 800; Best Local Similarity 63.2%; Pred. No. 0.24; Matches 55; Conservative 0; Mismatches 32; Indels (
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/310,357
FILING DATE:

APPLICATION NUMBER: US/08/310,357
FILING DATE:

APPLICATION NUMBER: US/07/904,075
FILING DATE:

APPLICATION NUMBER: EP 91.201.523.7
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: William M. Blackstone

REGISTRATION NUMBER: 29,772
REFERENCE/DOCKET NUMBER:

TELEBHONDIACTION INFORMATION:

TELEBHONDIACTION 
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STREET: 1300 Piccard Drive
CITY: Rockville
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APPLICANT: van den BOOGAART, Paul
APPLICANT: von den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
ADDRESSEE: Biotechnology Research Institute
STREET: 1330-A Piccard Drive
CITY: Rockville
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                                                                                                                                                                                                                                            COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08468852
Patent No. 5792644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA to mRNA INMEDIATE SOURCE:
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                                                                                                                                           STATE: Maryland
                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 20850
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US-08-310-357-7
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OCNUTION: IN PROCESSION OF STATEMENT OF STAT
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) OTHER INFORMATION: Description of Artificial Sequence: Reverse gene; OTHER INFORMATION: construct corresponding to a specific region of; JOTHER INFORMATION: the mouse Ii gene.
US-09-205-75
                                                                                                                                                                                                     20 ICCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Xu, Minzhen
APPLICANT: Qiu, Gang
APPLICANT: Humphreys, Robert
ITILE OF INVENTION: CANCER CELL VACCINE
FILE REFERENCE: US. Application 09/205,995, (CIP)
CURRENT FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, Minzhen
APPLICANT: Qiu, Gang
APPLICANT: Humphreys, Robert
IIILE OF INVENTION: CANCER CELL VACCINE
FILE REFERRNCE: U.S. Application 09/205,995, (CIP)
CURRENT APPLICATION NUMBER: US/09/205,995
CURRENT FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/036,746
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: 08/661,627
PRIOR FILING DATE: 1996-06-11
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09/036,746
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 72, Application US/09205995
; Patent No. 6368855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                              80 AAGGCT 85
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GENERAL INFORMATION:
APPLICANT: Xu, Minzhen
APPLICANT: Qiu, Gang
APPLICANT: Qiu, Gang
APPLICANT: Qiu, Gang
TITLE OF INVENTION: CANCER CELL VACCINE
FILE REFERENCE: U.S. Application 09/205, 995
CURRENT APPLICATION NUMBER: US/09/205, 995
CURRENT FILING DATE: 1998-12-04
FRIOR APPLICATION NUMBER: 09/036,746
FRIOR APPLICATION NUMBER: 08/661,627
FRIOR APPLICATION NUMBER: 08/661,627
FRIOR FILING DATE: 1996-06-11
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 75
ILENGTH: 107
  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 7.7%; Score 35.8; DB 2; 1 Similarity 63.2%; Pred. No. 0.24; 55; Conservative 0; Mismatches 32;
                                                                                                     PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/102,865
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/904,075
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 GCTGCTGCTGCCATGGTTCTTCAT 375
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                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,857
FILING DATE: 06-UTN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMALL.
ATTORNEY/AGENT INFORMALL.
NAME: NARY E. GOTMICH,
REGISTRATION NUMBER: 34,409
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 800 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 75, Application US/09205995 Patent No. 6368855
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ORGANISM: Artificial Seguence
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; LOCATION: 2..508
US-08-468-857-7
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Best Local Similarity
Matches 55; Conserv
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  SOFTWARE:
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No. 0.11; Matches 47; Conservative 0; Mismatches 19; Indels
Query Match
7.6%; Score 35.6; DB 4; Length 107;
Best Local Similarity 71.2%; Pred. No. 0.079;
Matches 47; Conservative 0; Mismatches 19; Indels
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PRIOR FILING DATE: 1998-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 182 RKKGSCCMWKKYYTYMRRRGGKWRSYKGGSCMCMMMMRGSCCSGGGGSCMWKSYKKWR 123
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                                                                                                                                                                                                                                                                                                                                                                                                            20 TCCCCCAAGCCCCTTTACCTATGCTGCTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTTA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 SYWRRRKYYYSRARGSYYMWKKTYMAARSCMRSSGGSMRGRARGGGKTYSGSCMMMRRR
                                                                                                                                                                                                                                                                                                                                                                    Gaps
PRIOR APPLICATION NUMBER: 08/661,627

PRIOR FILING DATE: 1996-06-11

NUMBER OF SEQ ID NOS: 79

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 77

IEMUTH: 190

TYPE: DNA

ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Reverse gene FRATURE:
OTHER INFORMATION: the mouse Ii gene.
US-09-205-995-77
                                                                                                                                                                                                                                                                                                                   7.6%; Score 35.6; DB 4; Length 190; 71.2%; Pred. No. 0.11; tive 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
7.6%; Score 35.4; DB 4; Length 430;
Best Local Similarity 12.7%; Pred. No. 0.22;
Matches 24; Conservative 92; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16656, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: GATCAINO, J.Y.
ITLLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054FR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 71.23
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GTGTCT 8
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LENGTH: 430
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Sequence 2, Application US/08553110 Patent No. 5723301 GENERAL INFORMATION:

US-08-553-110-2/c

RESULT 18

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APPLICANT: Kingsmore, Stephen
APPLICANT: Kingsmore, Stephen
APPLICANT: Tingsmore, Velizar
TITLE OF INVENTION: Insolation and Characterization of Hermansky-Pudlak
TITLE OF INVENTION: Interacting Proteins
FILE REFERENCE: 15966-523
CURRENT APPLICATION NUMBER: US/09/266,225D
CURRENT FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 4168
APPLICANT: Burke, James R.
APPLICANT: Vance, Jeffrey M.
APPLICANT: Langhild, Jan
APPLICANT: Explid, Jan
APPLICANT: Explid, Jan
APPLICANT: Explid, Jan
APPLICANT: Strittmatter, Warren J.
TITLE OF INVENTION: Therapeutics for Diseases Associated
TITLE OF INVENTION: with CAG Trinucleotide Repeat Expansion
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Drawer 34009
CITY: Charlotte
STREET: No. 5723301th Carolina
COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,110
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-266-225D-17/c
; Sequence 17, Application US/09266225D
Patent No. 6573364
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: 51.bley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFRENCE/DOCKET NUMBER: 5405-
TELEPONGUNICATION INFORMATION:
TELEPAN: 919-420-220
TELEPAN: 919-43175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1184 GGGTGGCGGTGGACTG 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 GACTGGTCGGTGCCCAG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1853 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-553-110-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-266-225D-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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41 TGCTGCTGCTAACGCTGCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGG 100
                                                       Gaps
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0
        Score 35.4; DB 4; Length 4168;
Pred. No. 0.92;
0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4279;
                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bradesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDICH TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.4; DB 3;
Pred. No. 0.94;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERNCK/POCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    1491 GGGTGGCGGTGGACTG 1475
                                                                                                                                                                               101 GACTGGTCGGTGCCCAG 117
           7.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4279 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California COUNTRY: United States
                                                  51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 239..3794
US-09-041-886-22
Query Match
Best Local Similarity
Matches 51; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                         US-09-041-886-22/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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1719 TGCTGCTGCTGCTGCTGTTGCTGTTGCTGGTGGTGATGGTGATGTGTTGAGACTGGT 1660

1659 GGGTGGCGGTGGACTG 1643

RESULT 21

101 GACTGGTCGGTGCCCAG 117

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41 TGCTGCTGCTAACGCTGCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGG 100

Gaps

0;

26; Indels

51; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Description of Unknown Organism: amyA gene
US-09-367-891A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 CCCCTTTACCTATGCTGCTAACGCTGCTGCTGCTGCTGCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                              APPLICANT: Gates, Krista
APPLICANT: Gates, Krista
APPLICANT: Wendland, Juergen
APPLICANT: Ayad-Durieux, Yasmina
APPLICANT: Dietrich, Fred
APPLICANT: Philipsen, Peter
TITLE OF INVENTION: Fungal Target Genes and Methods
FILE REFERENCE: PB/5-30908A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GACTGGTCGGTGCCCAGAAGTCTCTTCTGCCACTG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.2; DB 3;
Fred. No. 0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 GACTGATGTGAGCCCTGCTCCATGTATGCACTG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.5%; Score 35.2; DB 4;
83.3%; Pred. No. 0.92;
ttive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09367891A
Fatent No. 6524816
GENERAL INPORMATION:
APPLICANT: RASNUSSEN, PREBEN
TITLE OF INVENTION: EXPRESSION ELEMENT
FILE REFREENCE: 078883/0111
CURRENT APPLICATION NUMBER: US/09/367,891A
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: PCT/1898/00312
PRIOR PELLING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 5
IENGTH: 3311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/588,256 US/08/FILING DATE: 2000-06-05 NUMBER OF SEQ ID NOS: 24 SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 23
US-09-976-594-306/c
; Sequence 306, Application US/09976594
Sequence 1, Application US/09588256 Patent No. 6291665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%;
                                                           Gaffney, Thomas
Flavier, Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.4<sup>3</sup>
Matches 58; Conservative
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 83.3
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Ashbya gossypii
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (1)..(2160)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 22
US-09-367-891A-5/c
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
LENGTH: 2160
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                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                     189 GCCTCATCGGCCTGCCATGACCTGCAGCCCAGCCCCCGCGTGGGGAAGGGGAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                        Query Match 7.5%; Score 35.2; DB 1; Length 10807; Best Local Similarity 49.5%; Pred. No. 1.9; Matches 91; Conservative 0; Mismatches 93; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08756506
; Patent No. 5905185
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
APPLICANT: Temperley, Simon M.
APPLICANT: Foeter, Donald C.
; APPLICANT: Foeter, Donald C.
; APPLICANT: Prunkard, Donna B.
; TITLE OF INVENTION: RROTEIN C PRODUCTION IN TRANSGENIC;
; TITLE OF INVENTION: ANIMALS
; TITLE OF INVENTION: ANIMALS
; CORRESPONDENCE ADDRESSS:
; ADDRESSER: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/756,50
                                                                                                                                                                                         TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: ovine beta-lactoglobulin
       TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 9
TELECOMMUNICATION INFORMATION
                                                                                                                         LENGTH: 10807 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                 TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10807 base pai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206-442-6678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 GGGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                         US-08-206-176-7
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US-08-756-506-5
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Patent No. 6673549

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FULNES, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-041 US
CURRENT APPLICATION NUMBER: US/09/976,594
FRIOR APPLICATION NUMBER: 00/240,409
PRIOR PLING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SEQ ID NO 306
LENGTH: 9053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.5%; Score 35.2; DB 4; Length 9053; Best Local Similarity 54.9%; Pred. No. 1.7; Matches 67; Conservative 0; Mismatches 55; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Garner, Ian
APPLICANT: Garner, Ian
APPLICANT: Dalrymple, Michael A
APPLICANT: Foster, Donna E
APPLICANT: Foster, Donna E
APPLICANT: Foster, Donna C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 898877.6
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure

COCATION: 2006, 2012

CTHER INFORMATION: a, t, c, g, or other

US-09-976-594-306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 4225 Roosevelt Way, N.E CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08206176
Patent No. 5639940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZymoGenetics, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Parker, Gary E
REGISTRATION NUMBER: 31-
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1970 CT 1969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-206-176-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: S
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
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7.5%; Score 35; DB 3; Length 10348; 88.4%; Pred, No. 2.2;
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                                        for Huntington's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 TGCTGCTGCTAACGCTGCTGCTGCTGCTGCTGCTTAAAGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ross, Christopher
APPLICANT: Li, Xiao-Jiang
APPLICANT: Li, Xiao-Jiang
APPLICANT: Li, Shi-Hua
APPLICANT: Li anahan, Anthony
APPLICANT: Worley, Paul
APPLICANT: Worley, Paul
APPLICANT: Snyder, Solomon
TITLE OF INVENTION: Huntingtin-associated protein
FILE REFERENCE: 01107,52271.
CURRENT APPLICATION NUMBER: US/08/556,419C
CURRENT FILING DATE: 1995-11-09
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
GURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,273B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 2
Pred, No. 2.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                      APPLICANT: Nasir, Jamal
TITLE OF INVENTION: Mouse Model for Hunti:
TITLE OF INVENTION: Related DNA Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 10348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 3477-85A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-556-419-13/c
; Sequence 13, Application US/08556419C
; Patent No. 6093549
                                                                                                                                                                       CITY: Raleigh
STATE: No. 5849995th Carolina
COUNTRY: US
ZIP: 27627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 41:00
INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS:
LENGTH: 10348 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                   NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia Bennett
STREET: PO BOX 37428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
TELEPHONE: 919-854-1400
TELEFAX: 919-854-1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.5%;
Best Local Similarity 88.4%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
    APPLICANT: Lin, Biaoyang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                     8325 GGGIAAGCTGCCTGCCCTGCCCCACGTCCTGGGCACACATGGGGTAGGGGGTCTTGGT 8384
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                                                                                                                                                                                                                                                               8265 TGACTCTCCCTCCCCCACAGGGCAGTGCCACGTCTAGGTGAGCCCCCTGCCGGTGCCTCTG 8324
                                                                                                                                                                                                                                                                                                                                                                                              189 GCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCGTGGGGAAGGGGAAAGT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT PAPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER PILING DATE: 1998-07-02
EARLIER PILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 18
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 17
LENGTH: 176373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGCCIATCCACCICCCCCAAGCCCCTTTACCTAIGCTGCTGCTAACGCTGCTGCTGCTG
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                                                                                                                                   DB 2; Length 10807;
                                                                                                                                                                           93; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.5%; Score 35.2; DE 68.1%; Pred. No. 11; tive 0; Mismatches
                                                                                                                                                                           0; Mismatches
                                                                                                                                     Score 35.2;
Pred. No. 1.
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Patent No. 5849995
GENERAL INFORMATION:
APPLICANT: Rayden, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09128155
Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | NAME/KEY: misc_feature
| LOCATION: (1)...(176373)
| OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17
                                                                                                                                Query Match
Best Local Similarity 49.5%;
Matches 91; Conservative
LENGTH: 10807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 68.1%
....has 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIGCIGCIGCII 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                   ; TOPOLOGY: linear
US-08-756-506-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8445 GGTC 8448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 GGGC 312
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US-09-128-155-17
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US-08-453-265-5/c
; Sequence 5, Application US/08453265
; Patent No. 569375;
; Patent No. 569375;
; Patent No. 569375;
; APPLICANT: MacDonald, Marcy E.
; APPLICANT: Abborse, Christine M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
; VMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
; CITY: Washington
; STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 1; Length 10366;
Pred. No. 2.2;
0; Mismatches 5; Indels
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                                                    COUNTRY: U.S.A.

ZIP: 20005
COMPUTER: ELADABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: EN PC compatible
COMPUTER: DEAD TO STREET PC-DOS/MS-DOS
SOFTWARE: PATENTIAN BY 20, 1994
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
CLASSIFICATION: 438
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REFERENCE/DOCKET NUMBER: 29,021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEC ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10366 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3880003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.5%;
Best Local Similarity 88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
316..9748
CITY: Washington STATE: D.C.
                                                 U.S.A.
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US-08-246-982A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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Patent No. 5686288
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Ouyao, Mabel P.
APPLICANT: Gusella, James F.
TITE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
7.5%; Score 35; DB 3; Length 10348;
Best Local Similarity 88.4%; Pred. No. 2.2;
Matches 38; Conservative 0; Mismatches 5; Indels (
                                                                                                                                              WESULY.

WESULY.

US-00-12.9

US-00-12.9

Sequence 14, Application US/09041886

Patent No. 6238972

GENERAL INFORMATION:

APPLICANT: Bredesen, Dale E.

APPLICANT: Rabizadeh, Sharroz

TITLE OF INVENTION: Proapoptotic Peptides, Dependence

TITLE OF INVENTION: Polypeptides and Methods of Use

UNMBER OF ENQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: Callifornia

COUNTRY: United States

IP: 92122

COMPUTER: Floppy disk

COMPUTER: REDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: TBM PC Compatible

OPERATION TYPE: PO-DOS/MS-DOS

SOFTWARE: PAPLICATION DATA:

APPLICATION UNHER: US/09/041,886

FILING DATE:

CLASSIFICATION INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 9-LJ 2626

TELECOMMUNICATION INFORMATION:

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

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        41 IGCIGCIGCIAACGCIGCIGCIGCIGCIGCIGCITAAAGG 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 10348 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
316..9748
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US-08-246-982A-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-041-886-14
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Query Match
Best Local Similarity 68.6
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: 19.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-002-999-3
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STATE:
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APPLICANT: MacLeod Dr., Carol L.
ATILE OF INVENTION: No. 5312733el T-cell Lymphoma cDNA Clones
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         Score 35; DB 1; Length 10366; Pred. No. 2.2;
                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                 404 recrectecrecrecrecrecrecrecrecrecrecrecres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Patent Department, Fulbright & Jaworski STREET: 1301 McKinney, Suit 5100
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19910411
CLASSIFICATION: 435
                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/509684
FILING DATE: 13-APR-1990
ATTORNEY/AGENT INFORMATION:
NAMB: Launer, Charlene A.
REGISTRATION NUMBER: D-5232-CIP
TELEPHONE: (713) 651-3634
TELEPHONE: (713) 651-3634
TELEFAX: (713) 651-2646
TELEFAX: (713) 651-2646
TELEFX: Western Union 762829
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3819 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Gouble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SL12 cell line
                                                                                                                                                                                                                                                                                                                                                                                                      US-07-686-322A-3/c; Sequence 3, Application US/07686322A; Patent No. 5312733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE: Lymphoma
CELL TYPE: T-cell
CELL LINE: SL12.3 and SL12.4
IMMEDIATE SOURCE:
                                                                                                                                                                                                                       Query Match 7.5%;
Best Local Similarity 88.4%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
                                                LENGTH: 10366 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mouse
STRAIN: AKR1 Jackson
INDIVIDUAL ISOLATE: 8
                                                                                                                                              CDS
316..9748
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STATE: T.c..
COUNTRY: USA
T7010-3095
TADDEE F
                                                                                                               linear
                                                                         TYPE: nucleic STRANDEDNESS: TOPOLOGY: line
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                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-453-265-5
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                                                                                             Gaps
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APPLICANT: MacLecd Dr., Carol L.
APPLICANT: MacLecd Dr., Carol L.
TILLE OF INVENTION: No. 5440017el T-cell Lymphoma cDNA Clones
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Patent Department, Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.5%; Score 34.8; DB 1; Length 3819; Best Local Similarity 68.6%; Pred. No. 1.4; Matches 48; Conservative 0; Mismatches 22; Indels 0.
                                               DB 1; Length 3819;
                                                                                             22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 77010-3095
ZIP: 77010-3095
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                               7.5%; Score 34.8; D 68.6%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 53.0
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/686,322
FILING DATE: 11-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Benjamin A.
REGISTRATION NUMBER: 35,423
REFREENCE/DOCKET NUMBER: D-5232-DIV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: (713) 651-558
TELEX: (713) 651-558
TELEX: (713) 651-558
TELEX: (713) 651-558
SEQUENCE CHARACTERISTICS:
LENGTH: 3819 base pairs
TYPE: NUCLEIC ACID
TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SL12 cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUCH ASPLICATION DATA:
APPLICATION NUMBER: US/08/002,999
FILING DATE: 19930111
                                                                                                                                                                                                                                                                                                                                                                                  US-08-002-999-3/c; Sequence 3, Application US/08002999; Patent No. 5440017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN: AKRI Jackson
INDIVIDUAL ISOLATE: SL12 cell
TISSUE TYPE: Lymphoma
CELL IYPE: T-cell
CELL LINE: SL12.3 and SL12.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
     US-07-686-322A-3
     (202) 371-2600
TELEPHONE:
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GENERAL INFORMATION:
APPLICANT: Ranum et al.
ITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/056,170
EARLIER FILING DATE: 1997-08-19
NUMBER OF SEG ID NOS: 14
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                               Score 34.4; DB 3;
Pred. No. 0.43;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                   26 AAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTG
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                                                                                                                                                                                                                                                                                                               7.4%;
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Best Local Similarity 78.8°
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                TYPE: DNA ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-843A-1/c
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US-09-135-994-1/c
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Matches
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1862 IGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGAAACTGTTCGCTGGAACGTGG 1803
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Patent No. 5440491
GENERAL INFORMATION:
APPLICANT: KAKLZUKA, Akira
TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph Patent No. 5840491
TITLE OF INVENTION: Disease Gene and Uses Thereof NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 7.4%; Score 34.4; DB 2; Length 325; I Similarity 78.8%; Pred. No. 0.38; 41; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP H6-251600
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 35
US-09-253-691-3/c
; Sequence 3, Application US/09253691
; Patent No. 6124100
; GENERAL INFORMATION:
; APPLICANT: Dong Kyu JIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: ATT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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194
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                       1802 ATGATĠŤĠĠĠ 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Lexington
STATE: Massachusetts
                                                               101 GACTGGTCGG 110
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Best Local Similarity
Matches 41; Conserv
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IOCATION:
US-08-531-927B-3
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TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
FILE REPERENCE: 1942/36
CURRENT APPLICATION NUMBER: US/09/253,691
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: KR 98-6,278
EARLIER PILING DATE: 1996-02-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: WordPerfect 6.1/Windows
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 397;
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Patent No. 6514755

GENERAL INFORMATION:
APPLICANT Ranum et al.
TILE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: Regents of the University of Minnesota
CURRENT APPLICATION NUMBER: US/09/684,843A

CURRENT APPLICATION NUMBER: 60/056,170
PRIOR PILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                             Ouery Match 7.4%; Score 34.4; DB 4; Length 477; Best Local Similarity 60.9%; Pred. No. 0.49; Matches 56; Conservative 0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-481-814A-3/C
; Sequence 3, Application US/08481814A
; Patent No. 2869940
; GENERAL INFORMATION:
; APPLICANT: Hsu, Yen-Ming
; TITLE OF INVENTION: GENE THERAPY METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat_peptide
LOCATION: 3.1301
OCTHER INFORMATION: /function= "transcription factor"
OTHER INFORMATION: /product= "E2F-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,814A
                                                                                                                                                                                                                                                                                                          101 GACTGGTGCCCAGAAAGTCTCTGCC 132
                                                                                                                                                                                                                                                                                                                                                   101 eccecceccececececececreccccreae 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Cambridge
STATE: Massachusetts
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-679-2838
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH. 1332 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kaplan, Warren A
REFERENCE/DOCKET NUMBER: AC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2000
TELEFAX: 617-679-2838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens FEATURE:
                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-684-843A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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SEQ ID NO 1
LENGTH: 477
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                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION WINBER: US/08/886,582
FILING DATE: 14-MAY-1997
CLASSIFICATION DATA:
APPLICATION UNMBER: PCT/GB95/00868
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00868
FILING DATE: 18-APR-1995
PRIOR APPLICATION NUMBER: BCT/GB95/00868
FILING DATE: 18-APR-1995
PRIOR APPLICATION NUMBER: GB 9423049.7
FILING DATE: 15-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6303335th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1027 TTACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
                                                   Sequence 1, Application US/08836582; Sequence 1, Application US/08836582; Patent No. 6045998; Patent No. 6045999; Patent No. 6045999th General Information Sequence 1, APPLICANT: Bernards, Rene APPLICANT: Bernards, Rene TITLE OF INVENTION: Transcription factor E2F-4; NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESSE; ADDRESSE: Nixon & Vanderhye; STRETT: 1100 No. 6045999th Glebe Road, 8th Floor CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 TIACCIAIGCIGCIGCIAACGCIGCIGCIGCIGCIGCIGCI
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Patent No. 6303335
GENERAL INFORMATION:
APPLICANT: Bernards, Rene
APPLICANT: Berjersbergen, Roderick L
TITLE OF INVENTION: Transcription factor E2F-4
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 7.4%; Score 34.4; DB 3; Il Similarity 86.4%; Pred. No. 1; 38; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 62
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1489 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid_
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27..1268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 40
US-09-265-566-1/c
                                                                          RESULT 39
US-08-836-582-1/c
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US-08-836-582-1
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                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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34 TIACCTAIGCIGCIGCTAACGCTGCTGCTGCTGCTGCTGCTGCTGCT

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Sequence 871, Application US/09023655
Sequence 871, Application US/09023655
Retent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks Benjamin G.
APPLICANT: Cocks Benjamin G.
APPLICANT: Geffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS: 1508
STREET: 3174 FORTER DRIVE
CITY: PALO ALTO
STRATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 TTACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/WS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DAIR:
APPLICATION UNMBER: US/09/023,655
FILING DAIR: HERBWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.4%; Score 34.4; Di
Best Local Similarity 86.4%; Pred. No. 1;
Matches 38; Conservative 0; Mismatches
                             REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,011
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                              ; SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-242-737-3
                                                                                                                                                                                           LENGTH: 1489 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 871:
SEQUENCE CHARACTERISTICS:
LENGTH: 1489 base pairs
                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 27..1268
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 42
US-09-023-655-871/c
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TELEFAX: (
                                                                                                                                                                                                                                                                                              FEATURE
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ZIP: 22201-4714

COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   COMPUTER: IBM PC compatible
   OPERALING SYSTEM: PC-DOS/MS-DOS
   SOFFWARE: Patentin Release #1.0, Version #1.25 (BPO)
   CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/09/265,566
   FILING DATE: 1D-Mar-1999
   CLASSIFICATION: <UNKnown>
   15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BERNARDS, REN(
TITLE OF INVENTION: E2F UBIQUITINATION DOWAIN, AND ASSAYS FOR
INFIBITORS OF E2F UBIQUITINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
7.4%; Score 34.4; DB 4; Length 1489;
Best Local Similarity 86.4%; Pred. No. 1;
Matches 38; Conservative 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PATENTIN ROLES WAS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/242,737

FILING DATE: 23-PE-1999

CLASSIFCATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         991 TTACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
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                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/836,582
FILING DATE: cUnknown>
APPLICATION NUMBER: 08 9423049.7
FILING DATE: 15-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: ATTORNEY REGISTRATION NUMBER: 25,327
REGISTRATION NUMBER: 25,327
REPERENCE/DOCKET NUMBER: 620-18
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGTH: 1489 base pairs
TYPE: nucleic acid
STRANDENMESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/GB97/02293
FILING DATE: 22-AUG-1997
APPLICATION NUMBER: GB 9617697.9
FILING DATE: 23-AUG-1996
ATTORNEY AGENT INFORMATION:
NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 27..1268
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09242737
Patent No. 6368809
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-242-737-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
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APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Prospoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-LJ 2626
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; OTHER INFORMATION: Plasmid pGRO403R
US-08-479-913E-1
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 8-LJ
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9901
TELEFAX: (619) 535-8949
INFORMATION FOR SEG ID NO: 12:
SEQUENCE CHRARCTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08479913E Patent No. 6416998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear _ MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: O'Malley, Bert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
36..1116
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US-08-479-913E-1/C
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; LOCATION:
US-09-041-886-12
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US-08-531-927B-1/c

Sequence 1, Application US/08531927B

Patent No. 5440491

APPLICANT: KAKIZUKA, Akira

TITLE OF INVENTION:
Patent No. 5840491

TITLE OF INVENTION:
Patent No. 5840491

TITLE OF INVENTION:
Disease Gene and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.4%; Score 34.4; DB 2; Length 1776; Best Local Similarity 78.8%; Pred. No. 1.1; Matches 41; Conservative 0; Mismatches 11; Indels 0
                                               DB 4; Length 1489;
                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 23
CORRESPONDENCES: 23
CORRESPONDENCES: 23
CORRESPONDENCES: ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
CONFRY: USA
CONFRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
                                                                                                                                       34 TTACCTATGCTGCTGCTAACGCTGCTGCTGCTGCTGCTGCTGCT
                                                                                                                                                                                 994 AGGICCCGCIGCIGCIGCIGCIGCIGCIGCIGCIGCI
                                             Query Match 7.4%; Score 34.4; D
Best Local Similarity 86.4%; Pred. No. 1;
Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: ATH95-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9P H6-251600
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09041886
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: 36..1115
US-08-531-927B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-041-886-12/c
  US-09-023-655-871
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APPLICANT: Treat, Ming-Jer APPLICANT: Treat, Ming-Jer APPLICANT: Ledebur, Harry C. APPLICANT: Ledebur, Harry C. APPLICANT: Ledebur, Harry C. Tritle, Joseph D. TITLE OF INVENTION: MODIFIED STEROID HORMONES FOR GENE THERAPY AND METHODS FOR THEIR ITLING OF INVENTION: WOMBER: US/08/479,913E CURRENT FILING DATE: 1995-06-07 PRIOR REPELATION NUMBER: US 07/939,246 PRIOR FILING DATE: 1992-09-02 NUMBER OF SEQ ID NOS: 6 SOFTWARE: MicroSoft Word 97 SEQ ID NO 1 LENGTH: 6177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.4%; Score 34.4; DB 3; Length 1776; Best Local Similarity 78.8%; Pred. No. 1.1; Matches 41; Conservative 0; Mismatches 11; Indels 0
                                                                                                                                            ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Joha Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
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                                                                                                                          Hager Ph.D., Gordon L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MONITORING
DNA BINDING MOLECULES IN LIVING CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                APPLICANT: The Government of the United States of America as respresented by the Secretary Department of Health and Human Services Washington, D.C. Htun Ph.D., Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.4%; Score 34.4; DB 4; Length 7257; Best Local Similarity 78.8%; Pred. No. 2.7; Matches 41; Conservative 0; Mismatches 11; Indels 0
                                                                                    DB 4; Length 6177;
7.4%; Score 34.4; DB 4; Length 6: 78.8%; Pred. No. 2.5; cive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,042A
FILING DATE: 08-Jun-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Needle & Rosenberg
STREET: 127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Selby, Elizabeth
REGISTRATION NUMBER: 38.298
REFERENCE/DOCKET NUMBER: 14014.0183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1072..4284
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-091-042A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/008,373
FILING DATE: 08 Dec 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               US=09-091-042A-1/c
; Sequence 1, Application US/09091042A
; Patent No. 6455300
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 7257 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 404-688-9880 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 30303
COMPUTER READABLE FORM:
Query Match
Best Local Similarity 78.8
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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RESULT 47

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GENERAL INFORMATION:

APPLICANT: Bult et al.

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococomparter No. 6503729

TITLE OF INVENTION: jannaschii

TITLE OF INVENTION: NUMBER: US/08/916,421B

PRIOR PILING DATE: 1996-08-22

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.1
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                                                                                                                     APPLICANT: Ryan, James W.
APPLICANT: Ryan, James W.
APPLICANT: Pyrinkle, Terry Joe Curtis
APPLICANT: Pyrinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER PILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: SOFTWARE: SOFTWARE: PATENTING DATE: 10000
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c, or
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                              Sequence 4, Application US/09146053A Patent No. 6399349
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LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (28257) .. (28258)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
LOCATION: (84773) .. (84773)
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals
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CORGANISM: Homo sapiens
US-09-146-053-4
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US-08-916-421B-1/c
US-09-146-053-4
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KEY: misc_featur ION: (98159)(9 INFORMATION: n	: misc feat : (98239) FORMATION:	8c reacur 8266)(9 ATION: n	TEST TEST TEST (9) (9) (10) (10) (10) (10) (10) (10) (10) (10	ION: (103998)( INFORMATION: n	ION: (148948)( INFORMATION: n	EI: MISC ION: (1633 INFORMATI KRY: misc	ION: (191989)( INFORMATION: n	: (191995)( FORMATION: n	(231 (231 (231)	(234187)(   RMATION: n	(234 <u>7</u> 20)	misc reatu (234814) )RMATION: n	(86860	INFORMATION: n KEY: misc_featur	(309418) ORMATION: n	(312837) (RMATION: n	misc featur (312993)( DRMATION: n	misc_fea (319226) )RMATION:	misc fea (559167) ORMATION:	KEY: misc reacur ION: (559241)( INFORMATION: n	KEY: misc featur ION: (600 <u>9</u> 92)( INFORMATION: n	: misc_featur : (622708)( FORMATION: n	: misc featur : (657081)( FORMATION: n	NAME/KEY: misc feature LOCATION: (657203)(657203) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature

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LOCATION: (674435)(674435)  OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (682442)(682442)  OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (713652)(713652)  OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (741684)(741684)  OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a,	KEY: misc_feature_1 ION: (179455). (179455) INFORMATION: n equals a KEX: misc_feature ION: (179676). (179676) INFORMATION: n equals a KEY: misc_feature ION: (855539). (855539) INFORMATION: n equals a KEY: misc_feature	(8716 ORMATI misc (1084 ORMATI misc (1096 ORMATI		OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1349473)(1349473); OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1349491); OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1347091)(1470991); OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1470091)(1470091); OTHER INFORMATION: n equals a, NAME/KEY: misc feature	(1569) ORMATI misc (1603) ORMATI misc (1603) ORMATI misc (1617) (1617) (1664)

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318 TATTTAAAGTGGTTGTTTATGATTCTAATTTATACAAAGATATTAAAGGCCCTGT 377

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Query Match 7.4%; Score 34.4; DB 4; Length 1664976; Best Local Similarity 54.8%; Fred. No. 74; Matches 68; Conservative 0; Mismatches 56; Indels 0; G

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Sequence 1, Application US/08545528D

Patent No. 6537773

GENERAL INFORMATION:

APPLICANT: Fraser et al.

TILLE OF INVENTION: Nuclectide Sequence of the Mycoplasma Genitalium Genome, Fragment

Patent No. 6537773

TILLE OF INVENTION: Thereof, and Uses Thereof

PILE REFERENCE: P8193P1

CURRENT APPLICATION NUMBER: US/08/545,528D

CURRENT FILING DATE: 1995-10-19

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

SOFTWARE: PATENT NUMBER: US/08/473,545

NUMBER OF SEQ ID NOS: 1

SEQ ID NO 1

LENGTH: S80073
389857 TTTTTAACTGAGGGTATAATGACAATAACTCAAATGATAAGTGAGATTTTAATGCACAAT 389798
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                                                         378 TCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAA 437
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7.3%; Score 34.2; DB 4; Length 580073;
Best Local Similarity 52.4%; Pred. No. 49;
Matches 75; Conservative 0; Mismatches 68; Indels 0;
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ORGANISM: Homo sapiens
US-09-135-994-3
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US-08-545-528D-1/c
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Query Match

Search completed: May 25, 2004, 17:19:51 Job time : 101 secs

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2816.979 Million cell updates/sec
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                                                                                                                          May 25, 2004, 17:19:57; Search time 92 Seconds
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-863-639A-31
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US-09-621-976-91
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                                                                                                                                                                                                                                                                                                                                                                        682709 seqs, 277475446 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Listing first 100 summaries
                                                                                      OM nucleic - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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                                                                                                                                                                                                                SEQ29-NA-TRUNCATED 467
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1278 GAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGGTG 1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GGCTAGGGGGCCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 467; DB 4; Length 50000; 100.0%; Pred. No. 3.1e-223; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
FRALIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
ALIGNMENTS
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; Sequence 31, Application US/08863639A
; Patent No. 5981BS
; Patent No. 5981BS
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Rampal, Jang B.
                                                                                                          Sequence 4, Application US/09146053A
Patent No. 6399349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100. Matches 467; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                        RESULT 1
US-09-146-053-4/C
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 4
LENGTH: 50000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.4%; Score 25; DB 2; Length 36; Best Local Similarity 100.0%; Pred. No. 0.0046; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
TITLE OF INVENTION: OLIGONUCLECTIDE REPEAT ARRAYS
                                                              ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Detera-wadleigh, Sevilla D.
Gershon, Bliltot S.
Badner, Judith A.
Goldin, Lynn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 CGCTGCTGCTGCTGCTGCTGCT 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09091952A Patent No. 6458532 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
                                                                                                                                                                                                                                                                                                                                                                                                                  ATTONNEY/AGENT INFORMATION:
NAME: JOSEPH INFORMATION:
NAME: JOSEPH E. Musch
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11855
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEPHONE: (626) 795-6321
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                   COUNTRY:
                                                                                                                 CITY: F
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FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
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Best Local Similarity 100.
Matches 25; Conservative
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Matches 25; Conservative
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LENGTH: 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 37...63 COTHER INFORMATION: Clone 22 allele 2 polymorphic repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Detera-Wadleigh, Sevilla D.
Gershon, Elliot S.
Badner, Judith A.
Goldith A.
Goldith A.
Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic
Tests for Manic-Depressive Illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.4%; Score 25; DB 4; Length 91; Best Local Similarity 100.0%; Pred. No. 0.0047; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/029,278

FILING DATE: 28-0CT-1996

APPLICATION NUMBER: PCT/US97/19381

FILING DATE: 28-0CT-1997

ATTORNEY/AGRNT INFORMATION:

NAME: Smith, Timothy L.

REGISTRATION NUMBER: 35,367

REFERENCE/DOCKET NUMBER: 015280-297100US

TELECOMMUICATION INFORMATION:

TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
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                               CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: repeat region LOCATION: 37...63
         FILING DATE: 19-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                        TELEX: <UNKTOWN>
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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US-09-091-952A-14
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APPLICANT: DOING KYU JIN
TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
TITLE OF INVENTION: Using Trinuclectide Repeats Sequence
FILE REFERRNCE: 1942/36
FILE REFERRNCE: 1942/36
CURRENT FALING DATE: 1999-02-22
EARLIER FILING DATE: 1996-02-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: WordPerfect 6.1/Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: -
LOCATION: 1...94
OTHER INFORMATION: Clone 22 allele 1 polymorphic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone 22 allele 1 polymorphic repeat
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100.0%; Pred. No. 0.0049;
.ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.4%; Score 25; DB 4; Length 94; 100.0%; Pred. No. 0.0047; ive 0; Mismatches 0; Indels
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-0CT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prea. ...
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Patent No. 6124100
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 94 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 37...66
OTHER INFORMATION:
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Gaps
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STATE: VISIGNIA
ZIP: VA 22201-4714
CONDUTEX: US
ZIP: VA 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
RELING DATE: 14-Feb-2001
PRIOR APPLICATION DATA:
PRIDG DATE: 15-APR-1998
APPLICATION UNMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/043,553
FILING DATE: B-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: B-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: B-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: B-J.SAPATION:
NUMBER: B-J.SAPATION: NUMBER: US 60/048,740
FILING DATE: B-J.SAPATION: NUMBER: US 60/048,740
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STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
5.4%; Score 25; DB 4; Length 432
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 25; Conservative 0; Mismatches 0; Indels
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US-09-621-976-91/c
Sequence 91, Application US/09621976
Patent No. 663963
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
TITLE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 91
LENGTH: 570
TYPE: DNA
ORGANISM: Homo sapiens
Hey, Patricia
Kawaguchi, Yoshihiko
Merriman, Tony R
Metzker, Michael L
TITLE OF INVENTION: No. 6555654el LDL-Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCES: 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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REPERBUCE DOCKET NUMBER: 621
TELECOMPUNICATION INFORMATION:
TELEPHONE: (703)816-4091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703)816-4100 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: DEADEL FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: DEADEL FORM:

SOFTWARE: PATENTIN FC-DOS/MS-DOS

SOFTWARE: PATENTIN RATA:

APPLICATION NUMBER: US/09/060,299

FLING DATE: 15-APR-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/043,553

FILING DATE: 15-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/048,740

FILING DATE: 15-APR-1997

ATTORNEY/AGENT INFORMATION:

MAME: B.J.Sadoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 432;
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                                                                                                                                                                                                                                                                                                                                                                                                             AUURESSEE: Nixon and Vanderhye
STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.4%; Score 25; DB 4; I
100.0%; Pred. No. 0.0049;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                   APPLICANT: Hey, Patricia,
APPLICANT: Kawaguchi, Yoshihiko
APPLICANT: Kawaguchi, Yoshihiko
APPLICANT: Metzker, Michael L
TITLE OF INVENTION: No. 6545137el Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 cecrecrecrecrecrecrecrecr 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-35
TELECOMMULICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caskey, Charles T
Cox, Roger D
Gerhold, David
Hammond, Holly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09402923A; Patent No. 6555654; GENERAL INFORMATION:
                                                               Sequence 5, Application US/09060299
Patent No. 6545137
                                                                                                                                         Todd, John A
Hess, John W
Caskey, Charles T
Cox, Roger D
Gerhold, David
Hammond, Holly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Todd, John A
Hess, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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Matches 25, Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-09-060-299-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virginia
: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-402-923A-5
                                           JS-09-060-299-5
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Gaps
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US-08-531-927B-1/C
Sequence 1, Application US/08531927B
Fatent No. 584041
Fatent No. 5840491
Fatent No. 5840491
FAPLICANTE KARIZURA, AKITA
TILEOF INVENTION: DNA Sequence Encoding the Machado-Joseph
Fatent No. 5840491
FATENTESEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COMPTRY: Massachusetts
COMPTRY: Massachusetts
COMPTRY: Massachusetts
COMPTRY: BABDABLE FORM:
MEDIOK TYPE: Floppy disk
COMPTRY: BABDABLE FORM:
MEDIOK TYPE: PatentIn Release #1.0, Version #1.30
COMPTRY: 12-SEP-1995
COMPTRY: US/08/531,927B
FILING DATE: 21-SEP-1994
FILING DATE: 21-SEP-1994
ATTORNEY/AGSHT INFORMATION:
MAME: Granahan, Patriota
REGISTRAITON NUMBER: 32,227
REFERENCE/DOCKET                                                                                                                     ;
0
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                                                 Query Match 5.4%; Score 25; DB 4; Length 841; Best Local Similarity 100.0%; Pred. No. 0.005; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                               583 ścieciecieciecieciecieciecii 607
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; Sequence 12, Application US/09041886
; Patent No. 6215872
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bredesen, Dale E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1776 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36..1115
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FEATURE:
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; LOCATION:
US-08-531-927B-1
US-09-566-921-136
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Patent No. 6682886

GENERAL INFORMATION:

APPLICANT: Incirag, Jeanne F.

APPLICANT: Incirag, Jeanne F.

APPLICANT: Edwards, Carla M.

TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE;
FILE REFERENCE: PA-0024 US

CURRENT APPLICATION WUMBER: US/09/566,921

CURRENT APPLICATION WUMBER: US/09/566,921

CURRENT FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 138

SOFTWARE: PERL PROGRAM

SEQ ID NO 136

LENGTH: 841
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100.0%; Pred. No. 0.0049;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                     Query Match 5.4%; Score 25; DB 4; Length 570; Best Local Similarity 100.0%; Pred. No. 0.0049; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-621-976-2968/C

Sequence 2968, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: JODERT, S.

APPLICANT: Glordano, J.Y.

TITLE OF INFORTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION INVIERE: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm
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NAME/KEY: misc feature
NAME/KEY: misc feature
NAME/KEY: UNCOUNTION: Incyte ID No. 6682888 993585.1
NAME/KEY: UNCOUNTION: 610-611
OTHER INFORMATION: a, t, c, g, or other
      LOCATION: 355..570
INDEF/EXT: sig_peptide
LOCATION: 355..564
COTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 7.3000019073486
JCHER INFORMATION: seq YFLISILPLFTFR/GA
US-09-621-976-91
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Best Local Similarity 100.(
Matches 25; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 116..286
US-09-621-976~2968
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US-09-566-921-136
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Length 1884;
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Sequence 5, Application US/09398496

Fatent No. 613424

FARENEAL INFORMATION:

APPLICANT: Gearing, David P.

APPLICANT: Gearing, David P.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.4%; Score 25; DB 3; 18est Local Similarity 100.0%; Pred. No. 0.0051; Matches 25; Conservative 0; Mismatches 0
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX:
                                                                                                                                                                    07334/022001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
COUNTRY: US
ZIP: 0.210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIALE
OPERATING SYSTEM: DOS
SOFTWARE: FSSESSO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 CGCTGCTGCTGCTGCTGCTGCT 77
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/753,007
FILING DATE: 19-NOV-1996
APPLICATION NUMBER: 08/699,591
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: FASSE, J. Peter
REGISTRATION NUMBER: 32,983
                                                       08/699,591
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/69,59;
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: FASSE, J. PETER
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07334
TELECHMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Coding Sequence LOCATION: 664...1883
COTHER INFORMATION:
US-08-753-007A-5
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 1884 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 225 E
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            APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Campbell & Flores Lip
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bugfication US/08753007A
; Sequence 5, Application US/08753007A
; Patent No. 6074841
; GENERAL INCRMATION:
APPLICANT: Busfield, Samantha J.
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
; CITY: Boston
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUBBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-901
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    988 céchéchéchéchéchéchéchéch
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SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,007A
FILING DATE: 19-NOV-1996
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                                                                                                                                                                                                                COUNTY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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36..1116
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US-09-041-886-12
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Gaps

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RESULT 17
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J Sequence 6, Application US/09491522

Patent No. 6218999

Patent No. 6218999

PAPLICANT: Colige, Alain

APPLICANT: Lapiere, Charles M.

APPLICANT: Lapiere, Charles M.

TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,

TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds, LLP
                                                                                                                                                                                                                                                                                                                   ·.
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                                                                                                                                                                                                                                                                          Length 1884;
                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: Pennie & Edmonds, LLP
1155 Avenue of the Americas
New York
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APPLICATION NUMBER: 08/886,333
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REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAK: 650.493-5566
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2023 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                 NAME/KEY: Coding Sequence 10CATION: 664...1883
CTHER INFORMATION:
US-09-398-496-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1884 base pairs
                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                          MOLECULE TYPE: CDNA FEATURE:
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Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RY: USA
10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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53 CGCTGCTGCTGCTGCTGCTGCT 77

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US-08-261-822A-7/c
US-08-261-822A-7/c
Sequence 7, Application US/08261822A
Patent No. S650553
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R. et al.
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                        Sequence 13, Application US/09675305

Sequence 13, Application US/09675305

Patent No. 644153

GENERAL INFORMATION:

APPLICANT: Donobo, Gregory

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Triedrich, Glenn

APPLICANT: Friedrich, Glenn

APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and

TITLE OF INVENTION: Polynucleotides Encoding the Same

FILE REFERENCE: LEX-0047-USA

CURRENT APPLICATION NUMBER: US/09/675,305

CURRENT APPLICATION NUMBER: US 60/156,685

PRIOR FILING DATE: 1999-09-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: FLOEPY GLSA.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,822A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 2128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 GCIGCIGCIGCIGCIGCIGCTT 78
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TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2234 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: homo sapiens
US-09-675-305-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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RESULT 16
US-09-675-305-13
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Sequence 7, Application PC/TUS9507744A

GENERAL INFORMATION:
APPLICANT TRUETOR:
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.4%; Score 25; DB 5; Length 2234; 100.0%; Pred. No. 0.0051; ive 0; Mismatches 0; Indels
                                                                                                                                                                Length 2234;
                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFOUR TYPE: Floppy disk
COMPUTER FREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07744A
FILING DATE: 15-JUNE-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,822
FILING DATE: June 17, 1994
ATTORNEY/AGENT INFERMATION:
                                                                                                                                                           5.4%; Score 25; DB 1; 100.0%; Pred. No. 0.0051; ative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1973 Gerécrécrécrécrécrécrécrique
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REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3430
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2234 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
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                                    TOPOLOGY: linear
MOLECULE TYPE: CDNP
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                   ; ANTI-SENSE: NO
US-08-261-822A-7
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RESULT 19 US-09-491-522-2 ; Sequence 2, Application US/09491522

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Patent No. 6428998

GENERAL INFORMATION:
APPLICANT: College, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF NUMBER OF SEQUENCES: ...
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Pred. No. 0.0051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Mindows
SOFTWARE: FastESQ for Windows Version 2.0b
SOUREENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
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100.0%; Pred. No. c...
'... 0; Mismatches
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US-09-008-697A-13/C
Sequence 13, Application US/09008697A
Patent No. 6197504
GENERAL INFORMATION:
TITLE OF INVENTION: USES OF MAB-21
NUMBER OF EQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
CITY: New York
                                                                                                                                                                    SSES: Pennie & Edmonds, LLP
F: 1155 Avenue of the Americas
New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 838
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX: 650-493-5556
TELEX: 66141 PENNIB
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM Compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2450 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 25; Conservative
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Sequence 10, Application US/09521511C Patent No. 6555358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Todd, John A
Hess, John W
Caskey, Charles T
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cox, Roger D
Gerhold, David
Hammond, Holly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 25; Conservative
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                                         GENERAL INFORMATION:
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US-09-060-299-2
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548B1C1
CURRENT APPLICATION NUMBER: U5/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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100.0%; Pred. No. 0.0051;
iive 0; Mismatches 0; Indels
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5.4%; Score 25; DB 3; Length 2770;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           619 GCTGCTGCTGCTGCTGCTT 595
                                                        AUTORNEY AGENT INFORMATION:
NAME: Chan, Albert Wai-Kit
REGISTRATION NUMBER: 36,479
REFERENCE/DOCKET NUMBER: 50752-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2770 base pairs
TYPE: nucleic acid
STRANDEDNES; double
    APPLICATION NUMBER: US/09/008,697A FILING DATE: January 19, 1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 GCTGCTGCTGCTGCTGCTGCTT 78
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Patent No. 6642360
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferrara, Napoleone
Filvaroff, Ellen
Gerriteen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Conservative
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APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gurney, Austin
Hillan, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roy, Margaret
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Napier, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Homo Sapien
US-09-866-028-14
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 25; Conserv
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LENGTH: 3231
                                                                                                                                                                                                                                                                                                                                                 US-09-008-697A-13
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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RESULT 22 US-09-521-511C-10/c

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APPLICANT: Gurnett, Anne
APPLICANT: Gurnett, Anne
APPLICANT: Liberator, Paul A.
APPLICANT: Liberator, Paul A.
APPLICANT: Donaid, Robert
APPLICANT: Donaid, Robert
APPLICANT: Sattray, Sandra J.
TITLE OF INVENTION: CYCLIC GMP DEPENDENT PROTEIN KINASE AS A.
TITLE OF INVENTION: CYCLIC GMP DEPENDENT PROTEIN KINASE AS A.
TITLE OF INVENTION: CHEMOTHERAPEUTIC TARGET FOR ANTIPROTOZOAL AGENTS;
TITLE OF INVENTION: CHEMOTHERAPEUTIC TARGET FOR ANTIPROTOZOAL AGENTS;
TITLE OF INVENTION: 2036.2
CURRENT FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 4262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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100.0%; Pred. No. 0.0052;
tive 0; Mismatches 0; Indels
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SUFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,299
FILING DATE: 15-APR-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Nixon and Vanderhye
STREET: Nixon and Vanderhye
STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Vixolia
COMPURE: Use COMPURE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: COMPUTER: FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hey, Patricia
APPLICANT: Kawaguchi, Yoshihiko
APPLICANT: Merziman, Tony R
APPLICANT: Metzker, Michael L
TITLE OF INVENTION: No. 6545137el Receptor
UNIMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PULMASSIFICATION DATA:
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: US 60/048,740
05-JUN-1997
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Gaps
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                                                                                                                                Query Match 5.4%; Score 25; DB 4; Length 4843; Best Local Similarity 100.0%; Pred. No. 0.0052; Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: metzker, Michael L
APPLICANT: Metzker, Michael L
TITLE OF INVENTION: No. 65451376. Receptor
NUMBER OF SOUTHOURS: 455
CORRESPONDENCE ADDRESS:
ADDRESSER: Nixon and Vanderhye
STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.4%; Score 25; DB 4; I
100.0%; Pred. No. 0.0052;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IN PROCESSED COMPUTER: ENDOY disk COMPUTER: Floppy disk COMPUTER: Floppy disk COMPUTER: Floppy disk COMPUTER: Flat PC COMPATIBLE COMPUTER: Flat PC COMPATIBLE COMPUTER: ENDOY MATA: PAPLICATION DATA: APPLICATION NATA: APPLICATION NATA: APPLICATION NATA: APPLICATION NATA: APPLICATION NUMBER: US 60/043,553 FILING DATE: 15-APR-1997 PRIOR APPLICATION NUMBER: US 60/048,740 FILING DATE: 05-UN-1997 ATTORNEY/AGENT INFORMATION: NAME: B.J.Sadoff REGISTRATION NUMBER: 36,663 REFERENCE/DOCKET NUMBER: 620-35 TELECOMMUNICATION INFORMATION: TYPE: nucleic acid
STRANDENESS: single
TOPOLLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 CGCTGCTGCTGCTGCTGCT 77
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Cox, Roger D
Gerhold, David
Hammond, Holly
Hey, Patricia
Kawaguchi, Yoshiniko
Merriman, Tony R
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09060299 Patent No. 6545137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                f: 5098 base pairs
nucleic acid
bEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 5098 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Todd, John A
Hess, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 25; Conserva
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: US
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APPLICANT: Todd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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US-09-402-923A-2
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-060-299-1
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US-09-060-299-1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Feb-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                            5.4%; Score 25; DB 4; Length 4843; 100.0%; Pred. No. 0.0052; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metzker, Michael L
TITLE OF INVENTION: No. 6555654el LDL-Receptor
NUMBER OF SEQUENCES: 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/GB98/01102
PILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                           53 CGCTGCTGCTGCTGCTGCTGCT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caskey, Charles T
Cox, Roger D
Gerhold, David
Hammond, Holly
Hey, Patricia
Kawaguchi, Yoshihiko
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REFERENCE/DOCKET NUMBER: 62
                                                 REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-35
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFRA: (703)816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 decrecrecrecrecrecrecrecre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: VA 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09402923A
Patent No. 6555654
GENERAL INFORMATION:
APPLICANT: Todd, John A
Hess, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: B.J.Sadoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              LENGTH: 4843 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
US-09-060-299-2
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US-09-402-923A-2
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STATE: CA
COUNTRY: USA
ZIP: 94111-3834
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-09-491-522-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 28
US-09-091-952A-6
  APPLICANT:
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COUNTRY: US
ZIP: VA 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.4%; Score 25; DB 4; Length 5098; 100.0%; Pred. No. 0.0052; tive 0; Mismatches 0; Indels
                                                                                                                                                                                    APPLICANT: Todd, John A

Ress, John W

Caskey, Charles T

Cox, Roger D

Gerhold, David

Hammond, Holly

Hey, Particia

Kavaguchi, Yoshihiko

Merziman, Tony R

Merziman, Tony R

TITLE OF INVENTION: NO. 6555654el LDL-Receptor

NUMBER OF SEQUENCES: 455

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Feb-2001
PRIOR APPLICATION DATA:
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
APPLICATION NUMBER: US 60/048,740
ATTORNEY/AGENT INFORMATION:
NAME: B.J.Sadoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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80 CGCTGCTGCTGCTGCTGCTGCTTGCT 104
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                                                                                                                           ; Sequence 1, Application US/09402923A
; Patent No. 6555654
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09491522
Patent No. 6428998
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0°
Matches 25; Conservative
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                                                                                        RESULT 26
US-09-402-923A-1
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APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Darwin J.
TITLE OF INVENTION: RECOMBINAT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikwa, Takeo
Sanders, Alan R.
Esterling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic
Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6692;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows
SOFTWARE: FastESQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0060-999
TELECHONE: 650-493-4935
TELEFAX: 650-493-556
TELEFAX: 650-493-556
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6592 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 CGCTGCTGCTGCTGCTGCT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
FILING DATE:
                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
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Sequence 11, Application US/08068747

Patent No. 5695933

GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Housman, Thomas J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.1%; Score 24; DB 1; Length 30; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
                                                             CIP: 021/3

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 617-861-6240
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHRAACTERISTICS:
LENGTH: 30 base pairs

LENGTH: 30 base pairs
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusett
COUNTRY: USA
ZIP: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLA PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: DC-DOS/MS-DOS
SOFTWARING SYSTEM: DC-DOS/MS-DOS
SOFTWARING SYSTEM: DC-DOS/MS-DOS
SOFTWARING SYSTEM: DC-DOS/MS-DOS
ATPONDAY/DATE: 28-MAY-1993
CLASSIFICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATPONDAY/AGENT INPORMATION:
NAME: GRANADAN. PARTICIA
REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELEPRAK: 617-861-6240
TELEPRAK: 617-861-6240
TELEFRAK: 617-861-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 24; Conserva
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                                 COUNTRY: U
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US-08-068-747-11
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LOCATION: 5595...5685
OTHER INFORMATION: amplified region for genotyping
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 5.4%; Score 25; DB 4; Length 8065; Best Local Similarity 100.0%; Pred. No. 0.0053; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 452...505
OTHER INFORMATION: alternatively spliced portion
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: PastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 60/029,278

FILING DATE: 19-Apr-1996

APPLICATION NUMBER: PCT/US97/19381

PRING DATE: 28-OCT-1996

APPLICATION NUMBER: PCT/US97/19381

PILING DATE: 28-OCT-1997

ATTORNEY AGENT INFORMATION:

REGISTRATION NUMBER: 35,367

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 8065 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08068747
Sequence 6, Application US/08068747
Patent No. 5695933
GENERAL INFORMAT:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Hudson, Thomas J.
APPLICANT: Hudson, David Expanded
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 116...1036
OTHER INFORMATION: Clone 22 coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5634 écrécrécrécrécrécrécrécric
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LOCATION: 1...8065
OTHER INFORMATION: Clone 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 29
US-08-068-747-6/c
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GENERAL INFORMATION:
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US-09-684-843A-4/c
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                                                                                                                                                                                    SEQ ID NO 4
LENGTH: 30
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100.0%; Pred. No. 0.014;
tive 0; Mismatches 0; Indels
                                                                                                                                                5.1%; Score 24; DB 1; Length 30; 100.0%; Pred. No. 0.014; Live 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: Liskette, 3.50 inch, 1.44 Mb storage
COMPUTER: LibM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATIONTON: 435
                                                                                                                                                                                                                                                                                                                                                      Sequence 30, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Cassin, Peter J.
APPLICANT: Cassin, Peter J.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Sheldon & Mak
225 South Lake Avenue, 9th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: JOSEPh E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELEPHONE: (626) 796-4000
TELEPHONE: (626) 796-621
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 GCTGCTGCTGCTGCTGCTGCT 77
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                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: Other nucleic acid
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     30 base pairs
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STRANDEDNESS: sing
                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
Matches 24; Conserva
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US-08-863-639A-30/c
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US-09-135-994-4/c
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STATE: CA
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Sequence 4, Application US/09135994A Patent No. 6280938

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08570155
; Sequence 14, Application US/08570155
; Patent No. 5962332
; GENERAL INFORMATION:
    APPLICANT: Singer, Robert H.
    APPLICANT: Taneja, Krishan L.
    TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE REPEATS
    TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
    NUMBER OF SEQUENCES: 17
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ranum et al.
TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/056,170
EARLIER APPLICATION NUMBER: 60/056,170
BARLIER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 100.0
Matches 24; Conservative
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                                                                                                                                                                                                                         CRGANISM: Homo sapiens US-09-135-994-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 02110-2804
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ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 428, 1997
CLASSIFICATION: 428, 1997
REGISTRATION NUMBER: 20,532
REFERRACE/DOCKET NUMBER: 20,532
REFERRACE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION:
MANDER: 7068/MINICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Matson, Robert S.
APPLICANT: Cassin, Peter J.
APPLICANT: Cassin, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLECTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
SITRET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.1%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 24; Conservative 0; Mismatches
                                                                 06353/010WO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-863-639A-29; Sequence 29, Application US/08863639A; Patent No. 5981185; GENERAL INFORMATION:
               NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFRENCE/DOCKET NUMBER: 06353
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LILERANIE: (626) 796-400C
TELEFAX: (626) 795-400C
TELEFAX: (626) 795-6321
INPORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANNEDNESS: single
TOPOLOTY
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: CDNA PCT-US95-02861-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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MOLECULE TYPE:
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FGEUNCE 14/C
SEQUENCE 14, Application PC/TUS9502861
GENERAL INFORMATION:
FAPPLICANT: Singer, Robert H.
APPLICANT: Taneja, Krishan L.
TITLE OF INVENTION: BEPEATS
TITLE OF INVENTION: REPEATS
TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 225 Franklin Street
                                                                                   SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,155
FILING DATE: CLASSIFICATION DATA:
APPLICATION OF AN ENGLISH APPLICATION OF AN ENGLISH APPLICATION OF AN ENGLISH APPLICATION OF AN ENGLISH APPLICATION DATA:
APPLICATION NUMBER: 08/214,823
FILING DATE: 17 MARCH 1994
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKEY UNMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REJERENCE/DOCKEY UNMBER: 06353/011001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-6906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US95/02861
FILING DATE: 08 March 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/214,823
FILING DATE: 17 March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Wersion
SOFTWARE: #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 GCTGCTGCTGCTGCTGCTGCT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 GCTGCTGCTGCTGCTGCTGCTGCT
                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 542-8906
TELEX: 200154
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
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RESULT 39
US-09-043-14/C
Sequence 14, Application US/09043303
Fatent No. 6251589
GENERAL INFORMATION:
APPLICANT: SAUFEL, Shoji
APPLICANT: SAUFEL, Saujiro
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
TITLE OF INVENTION: Primers Therefor
FILE REFRENCE: 0760-0241P
CURRENT FILING DATE: 1998-05-18
EARLIER APPLICATION NUMBER: PCT/UP96/01999
BARLIER FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
FILE NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09043303
Patent No. 6251589
APPLICANT: SANPEI, Kazujiro
APPLICANT: SANPEI, Razujiro
FILE REFERENCE: 076-0241P
FILE REFERENCE: 076-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT PILING DATE: 1998-05-18
EARLIER PILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                 Score 24; DB 4;
Pred. No. 0.014;
                                                                           FEATURE:
CTHER INFORMATION: synthetic oligonucleotide
US-09-136-080E-50
                                                                                                                                                                                                                               8; Mismatches
                                                                                                                                                                                                                                                                                  54 GCTGCTGCTGCTGCTGCTGCT 77
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                                                                                                                                                                               5.1%;
  LENGTH: 53
TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                            Query Match
Best Local Similarity 66.74
Matches 16; Conservative
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COGANISM: Homo sapiens
US-09-043-303-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Hudson, Thomas J.
APPLICANT: Hudson, David E.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ANDERSS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1%; Score 24; DB 1; Length 51; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
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15 Sequence 50, Application US/09136080E

16 Sequence 50, Application US/09136080E

17 Sequence 50, Application US/09136080E

18 APPLICANT: Riley, Timothy A.

18 APPLICANT: Brown, Bob D.

18 APPLICANT: Arnold, Lyle J.

18 TITLE OF INVERTION: COMBINATORIAL ANTISENSE LIBRARY

18 FILE REFERENCE: OASHOLO,003A

19 CURRENT APPLICATION NUMBER: US/09/136,080E

10 URRENT FILING DATE: 1998-08-18

10 NUMBER OF SEQ ID NOS: 54

10 SOFTWARR: FaetSEQ for Windows Version 3.0

18 SEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: CB-MAY-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFO TANGER

NAME: Granahan, Patricia
REGISTATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
77
                                3 GCTGCTGCTGCTGCTGCTCT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 GCTGCTGCTGCTGCTGCTGCT 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
54 GCTGCTGCTGCTGCTGCTGCT
                                                                                                                                                                       Sequence 1, Application US/08068747 Patent No. 5695933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 51 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Militia [CITY: Lexington STATE: Massachusett COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
hes 24; Conserv
                                                                                                                                              US-08-068-747-1
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Matches
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Gaps

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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-043-303-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                       US-09-043-303-10/c

US-09-043-303-10/c

Sequence 10. Application US/09043303

Patent No. 6251589

Patent No. 6251580

APPLICANT: TSUJI.

APPLICANT: SANPEI.

TITLE OF INVENTION: Primers Therefor

TITLE OF INVENTION: Primers Therefor

TITLE OF INVENTION Primers Therefor

FILE REFERENCE: 0760-0241P

CURRENT APPLICATION NUMBER: US/09/043,303

CURRENT APPLICATION NUMBER: PCT/JP96/01999

SARLIER APPLICATION NUMBER: PCT/JP96/01999

SARLIER PILING DATE: 1996-07-18

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LENGTH: 75

HADGTH: 75

HADGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WS-09-043-303-11/c

| Sequence 11, Application US/09043303 |
| APPLICANT: SANDEL, Kazujico |
| TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and |
| TITLE OF INVENTION: Primers Therefor |
| TITLE OF INVENTION: Primers Therefor |
| TITLE OF INVENTION: Primers US/09/043,303 |
| CURRENT FILING DATE: 1998-05-18 |
| SEARLIER FILING DATE: 1996-07-18 |
| NUMBER OF SEQ ID NOS: 17 |
| SOFTHARE: Patentin Ver. 2.0 |
| SEQ ID NO 11 |
| LENGTH: 78
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100.0%; Pred. No. 0.015;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.1%; Score 24; DB 3; Length 75; Best Local Similarity- 100.0%; Pred. No. 0.015; Matches 24; Conservative 0; Mismatches 0; Indels
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                                          40 derecreerecreerecreer 17
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US-09-043-303-12/c
; Sequence 12, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
; APPLICANT: TSUJI, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CRGANISM: Homo sapiens
US-09-043-303-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRGANISM: Homo sapiens US-09-043-303-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and TITLE OF INVENTION: Primers Therefor FILE REFERENCE: 0.760-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
RAKLIER APPLICATION NUMBER: PCT/UP96/01999
RAKLIER FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Reverse gene; CTHER INFORMATION: construct corresponding to a specific region of; OTHER INFORMATION: the mouse Ii gene.
US-09-205-995-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Chung, Ming-yi
APPLICANT: CSgbbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 3; Length 78;
Pred. No. 0.015;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Xu, Minzhen
APPLICANT: Qiu, Gang
APPLICANT: Qiu, Gang
APPLICANT: Qiu, Gang
APPLICANT: Humphreys, Robert
ITILE OF INVENTION: CANCER CELL VACCINE
CURRENT APPLICANTION NUMBER: 09/09/205,995,
CURRENT FILING DATE: 1998-03-04
PRIOR APPLICATION NUMBER: 09/036,746
PRIOR APPLICATION NUMBER: 09/036,746
PRIOR APPLICATION NUMBER: 09/661,627
PRIOR APPLICATION NUMBER: 09/661,627
PRIOR FILING DATE: 1996-06-11
NUMBER OF SEG ID NOS: 79
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.1%; Score 24; DB 4; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 24; Conservative 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.1%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.0 Best Actions 24; Conservative 0; Mismatches
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; Sequence 6, Application US/08469802B
Patent No. 5741645
; GENERAL INFORMATION:
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Gaps

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Length 154;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
FILING DATE: 01-NOV-1994
FILING DATE: 01-NOV-1994
APPLICATION NUMBER: 08 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REGISTRATION NUMBER: 25,323
REGISTRATION NUMBER: 217211/M94/0434/GB
TELEPHONE: (202) 861-3000:
TELEPHONE: (202) 861-3000:
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.1%; Score 24; DB 2; Le:
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.1%; Score 24; DB 2; Le Best Local Similarity 100.0%; Pred. No. 0.015; Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-332-766A-13/c
iSequence 13, Application US/08332766A
Fatent No. 5843647
GENERAL INFORMATION:
APPLICANT: DEFFREYS, Alec J.
APPLICANT: ARMOUR, John
ITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUSHMAN DARBY & CUSHMAN, L.L.P.
                                                            110.00030120
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COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC comparible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATCHILI Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 GCTGCTGCTGCTGCTGCTGCT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1100 New York Avenue, N.W. CITY: Washington
     NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.0
TELEPCOMMUNICATION INPORMATION:
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1228
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 154 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 822-094
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 160 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-332-766A-13
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Patent No. 5834183
GENERAL INFORMATION:
APPLICANT: Crv. Harry T.
APPLICANT: Crung, Ming-yi
APPLICANT: Codung, Ming-yi
APPLICANT: Coghoi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.1%; Score 24; DB 1; Length 154; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A. STREET: P.O. Box 581415
CITY: Minneapolis
TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, STREET: 119 No. 5741645th Fourth Street, Suite 203 CITY: Mineapolis
STATE: MN
                                                                                                                                                                                      CUDNIKE: USA

CUDNIKE: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: PC-DOS/MS-DOS

COPFURE: IBM PC COMPATIBLE

COPFURE: DECENTING RELEASE #1.0, Version #1.25

SOFTWARE: PEPLICATION DATA:

APPLICATION NUMBER: US/08/469,802B

FLING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGBNT INFORMATION:

NAME: Muering, Ann M.

REGISTRATION NUMBER: 33,977

REFERENCE/POCKET NUMBER: 110.00030101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 Genecrecrecrecrecrecrecr 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 GCTGCTGCTGCTGCTGCTGCT 77
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MDDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 base pairs
TYPE: mcleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55458-1415
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                                                                                                                                                                            COUNTRY: USA
ZIP: 55401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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STATE: MR
COUNTRY:
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Gaps

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612-305-1225
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Best Local Similarity
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US-08-469-802B-4
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US-08-267-803B-4/c
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TELEFAX:
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                                                                                                                                                                                                                     APPLICANT: TSUJ, Shoji
APPLICANT: TSUJ, Shoji
APPLICANT: TSUJ, Shoji
APPLICANT: TSUJ, SANPEI, Kazujiro
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
TITLE OF INVENTION: Primers Therefor
FILE REFERENCE: 0760-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT APPLICATION NUMBER: PCT/JP96/01999
EARLIER APPLICATION NUMBER: PCT/JP96/01999
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Patent No. 5741645
GENERAL INPORMATION:
APPLICANT: Ranum, Laura P.W.
APPLICANT: Cound, Ming-Yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
ITLIE OF INVENTION: Type I and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Probe US-09-043-303-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.1%; Score 24; DB 3; Length 165; 100.0%; Pred. No. 0.015; ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTR:

ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING PATE: 06-UUN-1995
FILING PATE: 06-UUN-1995
FILING PATE: 06-UUN-1995
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TELECOMMUNICATION INFORMATION:
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    77
                                       105 GCTGCTGCTGCTGCTGCTGCT 82
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                                                                                                                                                        Sequence 17, Application US/09043303
Patent No. 6251589
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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Matches 24; Conservative
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                                                                                                                                       US-09-043-303-17/c
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Patent No. 5834183
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Chung, Ming-yi
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
TITLE OF INVENTION: Type 1 and Method for Diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.1%; Score 24; DB 2; Length 168; 100.0%; Pred. No. 0.015; or Indels iive 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
                                                                                                                                                                                                                                 5.1%; Score 24; DB 1; Length 168; 100.0%; Pred. No. 0.015; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Minneapolis
STATE: MN
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
CURRENT APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-UN-1994
CLASSIFICATION: 435
ATTORNEY/AGRNT INFORMATION:
NAME: MCCORMACK, MYTA H.
NAME: MCCORMACK, MYTA H.
REGISTRATION NUMBER: 36,602
REGISTRATION NUMBER: 36,602
REGISTRATION NUMBER: 36,602
REGISTRATION NUMBER: 31,00030120
                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. ...
Natches 24; Conservative 0; Mismatches
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TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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Search completed: May 25, 2004, 19:20:24 Job time: 94 secs

May 25, 2004, 16:30:32 ; Search time 3345 Seconds (without alignments) 6051.180 Million cell updates/sec 1 caatgtttgcctatccacct......taataaacagttaaaagctg 467 1846324 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 3470272 seqs, 21671516995 residues Post-processing: Listing first 100 summaries OM nucleic - nucleic search, using sw model OLIGO NUC Gapop_60.0 , Gapext 60.0 em_sy:* em_htgo_hum:* em_htgo_mus:* em_htgo_other:* em_vi:*
em_htg_hum:*
em_htg_inv:*
em_htg_other:*
em_htg_other:* SEQ29-NA-TRUNCATED 467 em_htg_pln:* em_htg_rod:* em_htg_mam:* em_htg_vrt:* Minimum DB seq length: 0
Maximum DB seq length: 200000000 gb ba:*
gb htg:*
gb_ntg:*
gb_om:*
gb_pt:*
gb_pt:*
gb_pt:*
gb_pt:*
gb_yt:*
gb_y em_ro:* em_sts:* em_un:* em_pat:* em_ph:* em_pl:* 10 Title: Perfect score: Sequence: Scoring table: Word size : Database :

Searched:

Run on:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Sequenc	Seque	Ношо	Homo	Seque	החחשבו	HOMO Sa	AAO//OO% SEQUENCE	HOMO SAD	AX332625 Sequence	Sequenc	Sequen	Primer	Homo s	Mus mu	Mus mus	Oryza sat	uman sı	Oryza	Comieno	oequemo	07779	AC017472 Drosophil	Oryzas	Mus mus	Medicago	Drosophi	AL954848 Zebrafish	Drosophi	Medicago		AC098642 Genomic s	Rattus no	Mus mus	Mus mus	AL929249 Mouse DNA	Mus mu	Mouse D	Mouse	Mus mus	Rattus	ACUSAZO/ KALCUS IIO	Mus mus	Rattus	Rattus	Rattus	AC131577 Mus muscu	AE003504 Drosophil	AF187994 Dipodomys	AY333192 Anopheles	Anopheres	GU9495 numan STS C	AY333201 ANOPHELES	Anophele	Anophele	Anophele	Fragari	AIISBUI3 FUCACEAE BC048870 Mus muscu	
SUMMARIES		AX092298	AX696953	AY358657	BC021104	AR211704	HS454M/	Ar195953	AAA / / 684 BD1 5 6 7 9 1	DX10072	AX332625	AX332852	AX874329		HUMZD38F03	AC122549	AC131317	AY023222	609506	ABOZBIB3	ANO 13848	A4634394 974357	CC423.4	AC017472	A2003411	AC103357	AC138056	AC010921	AL954848	AC012160	AC137828				AC132877	AC118589		AC12455	AL60368	AL60402	AC116661	AC131846	AC099207	AC127436 AC097480	AC125723	AC128474	AC125564	AC131577	AE003504		AY333192			AX333201 AY333003	AY333204	AY333205	AY333206	FVE508245	AY158013 BC048870	,
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U80893 Mus musculu BC012681 Mus muscul	U80889 Mus musculu	AY118433 Drosophil BC03632 Mus muscu	AĭUbU995 Drosophil AB090813 Anopheles	AC012983 Drosophil AF026032 Mus muscu	AC019984 Drosophil	Ar096/09 Drosophil AC019732 Drosophil	AL583932 Leishmani AC014982 Drosonbil	AY190934 Drosophil	AP005115 Oryza sat	AY190956 Drosophil	AC100911 Mus muscu AC019800 Drosophil	AC121129 Mus muscu	ACC20460 Drosophil	AX695800 Sequence	Magnap	Continuation (2 of		Acilyss Kattus no Continuation (2 of	Continuation (19 o AP005003 Oryza sat					linear PAT 21-MAR-2001			Craniata; Vertebrata; Euteleostomi;	i; Hominidae; Homo.	, Goddard, A., L., Watanabe C.K. and	and micleic acide						; Length 494;	58; 0; Indels 0; Gaps 0;	CTATGCTGCTGAGTAACGCTG 60	
5.6 1022 5.6 1048	5.6 1156 10		5.6 7072 3	5.6 7673 10	5.6 14532 2	5.6 25724	5.6 37891 2	5.6 38418 3	5.6 45375 5	5.6 46427	5.6 56366 2	5.6 65464	5.6 78964 2	5.6 79786	5.6 100500 2	5.6 110000 2	5.6 110000	5.6 110000 2 AC116234_1	5.6 110325 8 A	5.6 113887 5.6 114135		ALIGNMENTS			AX092298 AX092298.1 GI:13444463	Homo	Eukaryota, Metazoa, Chordata,	Mammalia; Eutheria; Primates; 1	<pre>Baton, D.L., Filvaroff, E., Gerritsen, M.E. Godowski, P.J., Grimaldi, C.J., Gurnev, A.L.</pre>	. [2	the same Patent: WO 0116318-1 20 00 MARS 2001	th, Inc. (US)	a)	/organism="Homo sapiens" /mol_type="unassigned DNA"	/db_xref="taxon:9606"	100.0%; Score 467	Similarity 7; Conservat	1 CAAIGTIIGCCIAICCACCICCCCCAAGCCCCTIIACCIAIGCIGAAAAAAAAAA	
		c 70 c 71		C 74	75	C 77			C 85		1 60	86 C 87		06 68	0 16 0 10			c 96	0 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	100			RESULT 1	AX092298 LOCUS DEFINITION	VERSION	SOURCE		REFERENCE	AUTHORS	TITLE	JOHNAL.	Sadiffaaa	Sanos		ORIGIN	Query Match	Best Local Matches 46	δλ	đa ,

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAA
                                                          181 TGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGGCCCCGGTGGGGAAGGG
                                                                                                                                             181 TGTCTCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCAGCCCCGTGGGGAAGGG
                                                                                                                                                                                     241 GAGAAAGTGGGGATGGCTAAGAAAGCTGGGAAATAGGGAAACAGAAGAGGGTAGTGGGTG
                                                                                                                                                                                                                                                    301 GGCTAGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAA
                                                                                                                                                                                                                                                                        361 AGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAATGITIGCCTAICCACCTCCCCCAAGCCCCTTTACCTAIGCTGCTGCTAACGCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Genentech Inc. (US)
Location/Qualifiers

    .494
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 495).

2 (lark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chini, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, T., Shigh, V., Satis, A., Vangts, A., Vanden, R., Vanden, R., Vanden, R., Vanden, R., Vanden, R., Vanden, R., Wiend, D., Woods, K., Kie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Goddwaki, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Befort to Identify Novel Human Secreted and Transmembrane Proteins:
                                                                                                                                                                                                                                                                                                                                                                                                        PRI 03-OCT-2003 complete cds.
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SFLCLLPHRPAMTCSQAQPRGEGEKVGDG"
                                                                                           GGCTAGGGGGGCCTGCCTTATTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAA 360
                                                                                                                                                         Bioinformatics, Genentech,
CA 94080, USA
                       TGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCCAGCCCCGTGGGGAAGGG
                                                                                                                                                                                                     AGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAA
                                                                   GAGAAAGTGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTG
 TGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAAGCCCCAGCCCCGTGGGGAAGGG
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Homo sapiens clone DNA56862 APELIN (UNQ471) mRNA,
AY358657
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Submitted (01-AUG-2003) Department of
Inc., 1 DNA Way, South San Francisco,
Location/Qualifiers
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Genome Res. 13 (10), 2265-2270 (2003)
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/organism="Homo sapiens"
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/db_xref="GI:37182436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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40. .261
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/note="PRO831"
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Homo sapiens (human)
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Length 495;

Score 467; DB 9; Pred. No. 2.3e-258;

100.0%;

Query Match Best Local Similarity

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ISM Home sapiens (numeau)

Four sapiens (numeau)

Fukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2673)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schemen,C.M., Schuler,G.D.,

Altschul,S.F., Jordan,H., Morce,T., Max,S.I., Wang,J., Hsieh,F.,

Biatcherko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Garninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

McKernan,K.J., Malleky,S.J., Bosak,S.H., McKwan,P.J.,

Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Fahey,J., Helton,B., Ketteman,M., Madan,A., Rodrigues,S.,

Sanchez,A., Whiting,M., Madan,A., Youug,A.C., Shevchenko,Y.,

Boutfaad,G.G., Ralaseley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,A., Scheut,E.D.,

Butterfield,Y.S., Krzywinsk,M.I., Skalska,U., Smailus,D.E.,

Generation and initial analysis of more than 15,000 full-length

Numer, Anners, Anners, Anners, Anners, M.A.,

Generation and initial analysis of more than 15,000 full-length
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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241 GAGAAAGTGG 2428 GAGAAAGTGG 301 GGCTAGGGGG 2488 GGCTAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	VERSTON KEYWORDS SOURCE UNKNOWN. ORGANISM Unclassified. REFERENCE TITLE Human aminopeptiase P gene JOURNAL FEATURES SOURCE LOCATION/Qualifiers 1.50000 /organism="unknown" CRIGIN KEYWORDS LOCATION/Qualifiers 1.50000 /mol_type="unknown"	Query Match 100.0%; Score 467; DB 6; Length 50000; Best Local Similarity 100.0%; Pred. No. 2.6e-258; Indels 0; Gaps 0; QY 1 Chargtraccrarccacracccraccccacacccraraccraraccraraccracaccracccracccracccracccracccracccracccracaccccracacccracacccracacccracaccccacaccccaccccaccccacccccaccccacccc	QY 181 TGTCTCTGCCTGCCTGCCATGACCTGCAGCCCAGCCCGTGGGGAAGGG 240 Db 1338 TGTCTCCTGCTCATCGACCTGCCATGCCCAGCCCCGTGGGGAAGGG 1279 QY 241 GAGAAAGTGGGCATGCTAAGAAGCTGCAGCTGCCCCGTGGGGAAGGG 1279 Db 1278 GAGAAAGTGGGGATGGTAAGAAGCTGGGAACAGAGGGGTAGTGGTG 1219 QY 301 GGCTAGGGGATGGCTAATTAAAGTGGTTGTTTATGATTTATACTAATTTATACAA 160 Db 1218 GGCTAGGGGGTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAA 1159 QY 361 AGATATTAAGGCCCTGTTCATTAAGATTGTTCCCTTCCC
TITLE Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gournal Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov This was procurement: DCTD/DTP COMMENT Email: gapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris F7ell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawar Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasha van den Bosch, Jill Vardy, George Yang, Sant	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 40 Row: f Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314667. FEATURES Location/Qualifiers 1. 2673 Organism="Homo sapiens" //organism="Homo sapiens" //db_xref="taxon:9606" //db_xref="taxon:9606" //clone="MGC:31846 IMAGE:4586949" //tissue type="Kidney, renal cell adenocarcinoma" //lab host="The NINH MGC 14"	note="Vector: porB7" 1 . 2673 2 dene="ApLN" db_xref="ApLN" db_xref="ApLN" db_xref="MiM:300297" 420.	Query Match 100.0\$; Score 467; DB 9; Length 2673; Best Local Similarity 100.0\$; Pred. No. 2.4e-258; 0; Gaps 0; 0; Atches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 0; QY 1 CAMTGTTTGCCTATCCACTCCCCCAAGCCCTTTACCTATGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC

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note="variant 1"
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Corresponding to the overlapping clone, as we submit sequences with This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSROT; Tr., TREMBL; Wp., WORMPEP information on the WORMPEP database can be found at thrp://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Futher://www.sanger.ac.uk/HGP/ChrxX RP3-4547 is from the library RPCI-3 constructed by the group of http://www.chori.org/bacpac/home.htm

WETOR: PUTHER: PUTHER: PUTHER: DECENTIAL SEGURD OF HTTP://www.chori.org/bacpac/home.htm
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3922. .4093,4621. .4735,5826. .5942,6041. .6228,9214. .9325,
10696. .10805,12706. .12841,18582. .18692,19339. .19504,
19759. .19994,30444. .30560,31621. .31705,32328. .32455,
33287. .33398 .35598)
                                                                         PRI 05-JUN-2003
                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 151152)
Pavitt, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 2, 1998 this sequence version replaced gi:2969945.
                                                               HS454M7 linear PRI 05-UUN-2:
Human DNA sequence from clone RP3-454M7 on chromosome Xq25-26.3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="dJ454M7.1.1 (Lowe Oculocerebrorenal Syndrome)"
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/mol type="genomic DNA"
/db_xref="RZPD:RPCIP704M07454"
/db xref="taxon:9606"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
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/clone lib≈"RPCI-3"
767. .35998
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                                                                                                                                                                              AL022162.1 GI:3171881
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                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                        complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: SC
                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                              Homo
                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
RESULT 6
HS454M7/c
                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
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JOURNAL
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match: ESTS: Em. AA366192 Em. AA704671 Em. AA515789
Em. AA4102623 Em. AA4126520 Em. AA704671 Em. AA515789
Em. AA4102623 Em. AA4126520 Em. T63686 Em. AA888434 Em. N02504
Em. AA4100629 Em. AA6186500 Em. T63686 Em. AA86650 Em. AA3034375
Em. AA100629 Em. AA6085500 Em. R94403 Em. AA66565 Em. AA4034375
Em. AA142870 Em. AA628152 Em. R849536 Em. AA4640853 Em. AA4189134
Em. AA64266 Em. AA740555 Em. RA878369 Em. AA640863 Em. AAA189134
Em. AA668822 Em. AA704555 Em. HE3971 Em. W88961 Em. AAA905220
Em. AA668822 Em. AA702176 Em. AA703474 Em. T84250 Em. H56932
Em. AA1869401 Em. AA188899 Em. HA188957
Em. W52373 Em. AA5889 Em. MA100630 Em. R88889 Em. H87857
                                                                                                                                                                                                                                                                                                                                                                                                             CROVISQLPRCHRIVVERVIMAFLRELLKFSEYNSVNANMIATLFTSLLLRPPPNLIMAR
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QTPSDRQRALGETLGSED"

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19759. 19994, 30444. 30560, 31621. 31705, 32328. 32455,
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MAVERGLENGARAKTKVQLYKLVGWMLLT FRAKOCKRITDLNTETVGTOFGNGKORNKG
GVAVREPHTTPCT TUNSHLAHVEDPERRADDYKDICARNSFEVFORDTFORGNING
EVVINLGDLNYRL.CMPDANEVKSLINKKDLQRLIKFDQLNIQRTQKKAFVDFNBGEIX
FTH TYKTXDRXDRNADSGRCKRVPAMCDTRILMFGTONYRQLNYRSHMELKTSDHKFVSAL
FHIGWKVVDERRYRKVFEDSYRINDRNBSNPFLPSLELSRREFVFENVKFRQLQKEKFO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="CCKIRYQGDWIRERRFEIPDEEHCLKFLSAVLAAQKAQSQLLVP
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CLDTSIPETIPGSNHSVABALLIFLEBALPEPVICYELYQRCLDSAYDPRICROVISOL
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match: cDNAs: Em:M88162 Em:U57627 Em:M74161 Em:AF040094 match: ESTs: Em:AA368192 Em:AA704671 Em:AA515789
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/hote="MIR repeat: matches 2. .262 of consensus"
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Qy 181 TGTCTCCTGCCTCATCGGCCTGCCATGACCTGCAGCCCAGCCCGTGGGGAAGGG 240 Bb 89538 TGTCTCCTGCTCATCGGCCTGCCATGCCCAGCCCGTGGGGAAGGG 89479 Qy 241 GAGAAAGTGGGGATGGCTAAGAAAGTGGGAATAGGGAACAGAGGGTAGTGGGTG 300 Bb 89478 GAGAAAGTGGGGATGGCTAAGAAAGTGGTGGTGTGTATAATAATAAAAAGTGGTAGTGGTG	AF195953 AF195953 Homo sapiens membrane-bound aminopeptidase P (XNPEP2) AF195953 AF195953 AF195953 AF195953 AF195953. Gill9718557 Homo sapiens (human) Homo sapiens (huminidae; homo sapiens (huminidae; huminidae; homo sapiens (huminidae; huminidae; humini	mRNA join(144189: 144502,147348. 147421,149203. 149313, 150445. 150508,15148. 151582,15187. 151923, 152849. 152995,155710. 155811,156897. 157068, 157392. 157587,158401. 158490,155714. 15983, 160536. 160513,161726. 1617248. 157382, 16736. 1668012,172845. 172934,173533. 176791) /gene="XRRPEP2" /product="membrane-bound aminopeptidase P" /gene="XRRPEP2" CDS join(14454. 14452,1478. 15182,151837. 151923, 150445. 1550508,151478. 15182,151837. 151923, 157392. 157587,158401. 1588490,155714. 155982, 166536. 160613,161726. 1614922. 164482.
region	repeat_region 1539. 15599 repeat_region 16139. 16299 at: matches 1. 311 of consensus" repeat_region 16139. 16299 peat: matches 1. 209 of consensus" repeat_region 16139. 1629 peat: matches 1. 209 of consensus" repeat_region 16139. 1629 peat: matches 29. 178 of consensus" forte="WIRTS repeat: matches 52. 212 of consensus" forte="WIRTS repeat: matches 52. 212 of consensus" forte="WIRT repeat: matches 52. 212 of consensus" forte="WIRT repeat: matches 5491. 5829 of consensus" forte="WIRT repeat: matches 5491. 5829 of consensus" forte="WIRT repeat: matches 6. 242 of consensus" forte="WIRT repeat: matches 6. 242 of consensus" forte="WIRT repeat: matches 6. 242 of consensus" forte="WIRT repeat: matches 1. 150 of consensus" forte="WIRTS repeat: matches 1. 150 o	Query Match 100.0%; Score 467; DB 9; Length 151152; Best Local Similarity 100.0%; Pred. No. 2.7e-258; Additional State of Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 CAATGTTTGCCTATCCACTCCCCCAAGCCCCTTTACCTATGCTGCTGCTGCTG 60 Db 89718 CAATGTTTGCTATCCACTCCCCCAAGCCCTTTACCTATGCTGCTGCTGCTG 89659 Qy 61 CTGCTGCTGCTTAAAGGCTCATGCTTGAGTGGGGACTGGTGCTGCTGCTGAAA 120 Db 89658 CTGCTGCTGCTTAAAGGCTCATGCTTGAGTGGGGACTGGTGGTGCTGGTGCTGAAA 89599 Qy 121 GTCTTTCTTGCTGAGTGCCCCATCAGGATTGGGCCTTCTTTTTTG 180 Bb Qy 121 GTCTTTTTTCTGAGTGCCCCATCAGGATTGGGCCTTCTTTTTTTT

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Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primers for synthesising full-length cDNA and their use
Patent: EP 1074617-A 12589 07-FEB-2001;
Research Association for Biotechnology (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="Cae89834.1"
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                                                                                                                                                 PAT 17-DEC-2003
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                                                                                                                                                                                                                                                        Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                            51098 AGATTCTTCTGTGTAAATATGTCTTTATAATAAGAGTTAAAAAGCTG
        AGATTGTTGTGTAAATATGTCTTTATAATAAACAGTTAAAAGCTG
                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product"
                                                                                                                               AX877684 2243 bp DNA
Sequence 12589 from Patent BP1074617.
AX877684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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        421
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Best Local S:
Matches 413
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VERSION
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BDESGAET VUKRRGEEQFSSGPSFETI SASGLNAALAHYSPTKELNRKLSSDEMYLLD
SGGQYWDGTTDI TRTVHWGTPSAFORRAYTRYLIGNIDLSRLI FPAATSGRWTBAFAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                    /note="putative proton shuttle; unclassified site" 161778. .161780. /gene="XNBF2" /fone="Alberg" metal ligand; metal-binding site" 164435. .164437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="divalent metal ligand; metal-binding site"
166473. .166475
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/gene="XNPEP2"
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  .166518,167248. .167307, .172934,173533. .173727)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="divalent metal ligand; metal-binding
join(167307,167936..167937)
/gene="XNBFD2"
/note="divalent metal ligand; metal-binding
167977..167979
                                                                            ቪ
                                                                      /product="membrane-bound aminopeptidase
/protein_id="AAG28480.1"
/db_xref="GI:11066157"
. .165823,166414.
. .168012,172845.
                                                                                                                                                                                                                                                                                                                                                               160606. .160608
/gene="XNPEP2"
                                  gene="XNPEP2"
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Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mall:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human CDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Centerection: and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="g1:7023383"
/fb_xref="g1:7023383"
KGPPSAHPLRICTLHRIVORSGUTSIQLSPRICCSHQWAQLFSPACFPQWRAPGCSL
DDSRSLTRIREVHHESPSCD"
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                                                                                                                                                                                                                                                                               Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Namase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A.
                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (16-FBB-2000) Takao Isogai, Helix Research Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'tissue type="placenta"
'clone lib="PLACE1"
'note="cloning vector: pME18SFL3"
                                                                              oligo capping, fis (full insert sequence).
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6. .374
/note="unnamed protein product"
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/organism="Homo sapiens"
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/protein_id="BAA91944.1"
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/db_xref="taxon:9606"
/clone="PLACE1002140"
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Location/Qualifiers
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gai, T. and Otsuki, T.
                                                  AK001855.1 GI:7023382
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Matches 413; Conservative
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(bases 1 to 2243)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Makamatsu,A., Nagai,K. and Otsuki,T. Primar for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 11634 09-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMAWSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
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Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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   Primer for synthesizing full-length cDNA and use thereof
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Location/Qualifiers
1. .2243
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
JP 2002191363-A/11634
09-JUL-2002
28-JUL-2000 JP 2000280990
                                                            BD156791.1 GI:27862549
JP 2002191363-A/11634.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                  252 CCCGTGGGGAAGGGGGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGAACAGAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGAGAAAGTGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGGTAGTGGG 170
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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51.0%; Score 238; DB 6; I
Best Local Similarity 99.7%; Pred. No. 7.5e-126;
Matches 288; Conservative 0; Mismatches 1;
                    13-DEC-2001;
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                                                                                                             /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                              sapiens"
              Patent: WO 0194629-A 3361 13-
Avalon Pharmaceuticals (US)
Location/Qualifiers
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/organism="Homo
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2131 ATACAAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGT 2190
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Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
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                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                      415 TIGIAAAGAIIGIICIGIGIAAAIAIGICITIAIAAIAAACAGIIAAAAGCIG
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Location/Qualifiers
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Gaps

PRI 29-AUG-1998

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Direct Submission
Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted
                                                                                                                                                                                                                                                                                                    1 (bases i to 598)
Woessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,
Woessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,
Marth,G., Bowles,L., Wylle,T., Bowers,Y., Steptoe,M., Thaising,B.,
Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B.,
Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behymer,K., Hillier,L.,
Wilson,R. and Waterston,R.
Full Clone Sequencing of the Longest Available Member from Each
Unique Cluster
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                                                                                                                                                                                                                                                             Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the full insert of this cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 ICTIATACTAATTTATACAAAGATATTAAGGCCCCTGTTCATTAAGAAATTGTTCCCTTCC
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                                                                           השהעם mRNA linear 598 pp mRNA linear Homo sapiens full length insert cDNA clone ZD38F03.
AF086248
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/clone_lib="Soares_fetal_heart_NbHH19W"
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Best Local Similarity 100.0%; Pred. No. 1.3e-61;
Matches 127; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu
                                                                                                                                                           AF086248.1 GI:3483593
                                                                                                                                                                                  FLI_CDNA.
Homo sapiens (human)
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Waterston, R.
                                                                                                                                                                                                                                 Homo sapiens
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HUMZD38F03
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(bases 1 to 403)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishi,S., Sujiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for synthesizing full-length cDNA and use thereof Patent:

(pr 2002191363-A 9234 09-JUL-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HELIX RESEARCH INSTITUTE

S Home sapiens (human)

PD 2002101363-A/9234

PD 09-JUL-2000 JP 2000280990

PI 70SHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU

PI SALTO,

PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,

PI KEIICHI NAGAI, TETSUJI OTSUKI

OCILINIS/09, CO7K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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359 AAAGATATTAAGGCCCTGTTCATTAAGAAATTGTTCCCTTCCCTGTGTTCAATGTTTGT 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 GGGAGAAAGTGGGGGGATGGCTAAGAAAGCTGGGAGAATAGGGAAACAGAAGAGGGTAGTGGG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 TGGGCTAGGGGGGCTGCTTATTAAAGTGGTTGTTTATGATTNTTATACTAATTTATAC 110
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Primer for synthesizing full-length cDNA and use thereof.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                           BD154391.1 GI:27860149
JP 2002191363-A/9234.
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Homo sapiens
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                                                      AC122549 202198 bp DNA linear HTG 13-MAR-2003
Mus musculus clone RP23-406024, WORKING DRAFT SEQUENCE, 9 unordered
pieces.
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 202198)
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-406024
                                                                                                                                                                                   AC122549.4 GI:28933870
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                             Mus musculus (house mouse)
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                         15814: contig of 3052 bp in length 15914: gap of 100 bp 27843: gap of 11929 bp in length 27843: gap of 1100 bp 100820: contig of 72877 bp in length 17522: contig of 71602 bp in length 172622: gap of 100 bp 201198: contig of 29576 bp in length 201198: contig of 29576 bp in length
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of 3052 bp in length
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/clone="tayon"
/clone="tayon
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Web site: http://www-seq.wi.mit.edu
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/note="assembly_fragment"
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'note="assembly_fragment"
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72623. .202198
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------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                     On Mar 21, 2003 this sequence version replaced gi:28412031.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 198000; agarose-fp
Insert size: 203371; sum-of-contigs
Quality coverage: 8.9 in Q20 bases; agarose-fp
Quality coverage: 8.7 in Q20 bases; sum-of-contigs
                                                  All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: 126954

Center clome name: 333 F 2

Center clome name: 338 F 2

Sequencing vector: Plasmid, n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 202347 bases at least Q40

Consensus quality: 202846 bases at least Q20

Consensus quality: 202986 bases at least Q20
                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4: contig of 61474 bp in length
4: gap of 100 bp
9: gap of 100 bp
4: contig of 2905 bp in length
4: gap of 100 bp
1: contig of 4685 bp in length
1: contig of 16687 bp in length
1: gap of 100 bp
0: contig of 19479 bp in length
0: gap of 100 bp
2: contig of 19479 bp in length
0: gap of 100 bp
2: contig of 19479 bp in length
0: gap of 100 bp
2: contig of 19471 bp in length
1: gap of 100 bp
2: gap of 100 bp
3: gap of 100 bp
4: contig of 19471 bp in length
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of 58698 bp in length
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2 202881: gap of 100 bp
12 204171: contig of 1290 bp in length.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
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/note="assembly_fragment"
124513. .143983
/note="assembly_fragment"
144084. .202781
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/note="assembly_fragment"
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/db_xref="taxon:10090"
/clone="RP23-333F2"
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                COMMENT
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Bodsalavkiy, L., Boukhgalter, B., Camaraca, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Gardyna, S.,
Graham, J., Grand-Pierre, N., Hagez, N., Gardyna, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabtier, R., MacCeanth, N.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, N.,
Meldrim, J., Meneus, L., Minowa, T., Matthews, C., McCarthy, N.,
Neldrim, J., Meneus, L., Minowa, T., Menga, V., Murphy, T., Naylor, J.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raywond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovitc, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B.,
Nyman, D., Young, G., Zalnoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (21-MAR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG 21-MAR-2003
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Mus musculus clone RP23-333F2, WORKING DRAFT SEQUENCE, 9 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 204171)
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                                                                                                                                                                              Gaps
                                                                                                                                                                         ·.
                                                                                Query Match 6.0%; Score 28; DB 2; Length 202198; Best Local Similarity 100.0%; Pred. No. 0.00031; Matches 28; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                     104108 TAACGCTGCTGCTGCTGCTGCTGCTGCT 104135
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                                                                                                                                                                                                                                             50 TAACGCTGCTGCTGCTGCTGCTGCT
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Mus musculus (house mouse)
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seq29-na-truncated.olig10.rge

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PLN 22-JAN-2000
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Oryza sativa
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                          1 (bases I to 373)
Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H.
Coperative Human Linkage Center
Unpublished (1998)
Synonyms: GCT4601, CHLC.GCT4601.T10965
Contact: Dr. Jeffrey C. Murray
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xikuchi, K., Ueguchi-Tanaka, M., Yoshida, K.T., Nagato, Y., Matsusoka, M. and Hirano, H.Y.
Matsusoka, M. and Hirano, H.Y.
Molecular analysis of the NAC gene family in rice
Mol. Genet. 262 (6), 1047-1051 (2000)
20123461
                                                                                                                                                                                                                                                                                                                                                             30 seconds at 94 degrees C
75 seconds at 55 degrees C
15 seconds at 72 degrees C
27
                                                                                                                                                                                                                                                                                                                                                                                                                                      6 minutes at 72 degress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB028183 1264 bp mRNA linear Oryza sativa mRNA for OSNAC4 protein, complete cds.
                                                                                                                                                            The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30ng genomic DNA
each 1.5 pmole
each 200 uM
0.3 units
10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.8%; Score 27; DB 11; I Best Local Similarity 100.0%; Pred. No. 0.00096; Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                              Primer A: TGCGGGTAAAAGATGAPrimer B: ACTCTAGGAATGAGAATGCG
STS size: 106
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 CGCTGCTGCTGCTGCTGCTGCTTA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 CGCTGCTGCTGCTGCTGCTTA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taq Polymerase:
Total Vol:
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complement(96. .117)
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Location/Qualifiers
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50mM
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extension:
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extension:
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OBNAC4; OSNAC4 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protocol:
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                                                                                                                                                                                                                                                                                                                                    227 bp DNA linear PLN 07-FEB-2001
Oryza sativa microsatellite MRG5547 containing (GCT)X9, closest to
marker L825, genomic sequence.
AY023222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tao,N., Barbazuk,W.B., Liu,J., Wu,K. and Barry,G.F.
Tao,N., Barbazuk,W.B., Liu,J., Wu,K. and Barry,G.F.
Direct Submission
Submitted (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh
Blvd., Creve Coeur, MO 63167, USA
Derived from rice genomic sequences generated from the Monsanto
Rice Genome Sequencing project. Please see
http://www.rice-research.org for more information. The sequence
data were produced primarily in the laboratories of Dr. Leroy Hood
at the University of Washington in Seattle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa bukaryota; Embryophyta; Tracheophyta; Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryza.

1 (Dases 1 to 227)

1 (Dases 1 to 227)

Simple sequence repeats from Monsanto rice genomic sequences Unpublished
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human STS CHLC.GCT4G01.P10966 clone GCT4G01, sequence tagged site.
G09506
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STS; STS sequence; primer; sequence tagged site.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                Gaps
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                                                                                                                                   6.0%; Score 28; DB 2; Length 204171; larity 100.0%; Pred. No. 0.00031; Conservative 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 0.00094;
ive 0; Mismatches 0; Indels
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/mol_type="genomic DNA"
/db_zref="taxon:4530"
1. .227
/note="microsatellite MRG5547"
                                                                                                                                                                                                                                               53830 GCTGCTGCTGCTGCTGCTTAAA 53857
/note="assembly_fragment"
                202882. .204171 /note="assembly_fragment clone_end:T7 vector_side:right"
                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 AACGCTGCTGCTGCTGCTGCTGCT 124
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                                                                                                                                                                                                               54 GCTGCTGCTGCTGCTGCTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_type=tandem
/rpt_unit="gct"
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                                                                                                                                                      Similarity
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                    misc_feature
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Matches 28;
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2. (Dages I to 1283)
2. (Dages I to 1283)
3. Adachi J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, K., Hanagaki, T., Hara, A., Hashizume, M.,
Fujimura, T., Fukuda, K., Hanagaki, T., Hara, Hashizume, M.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Himamura, K.,
Imotrani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itch, M., Kagawa, I.,
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozame, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, Y., Kojima, Y., Kojima, Y., Kolano, H., Kouda, M.,
Kodama, T., Kojima, Y., Murakami, Y., Mura, J., Miyazaki, A.,
Masuda, H., Matsubara, K., Maceuyama, T., Miura, J., Miyazaki, A.,
Mizuno, K., Murakami, K., Murata, M., Nishi, K., Nomura, M.,
Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ocka, H.,
Sakazume, N., Sano, H., Sasaki, D., Satoh, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sujiyama, A., Suzuki, Y., Tagami, M., Tagami, Takeda, Y.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Towan, Y., Yokomizo, S. and
Vochimura, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FALS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., FALS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Kurosaki,T., Kusumegi,T., Lu,M., Masuaki,M., Mizua,J., Mizuno,K., Marikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken Genomic Sciences Center Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hangawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hangari,T., Hara,A., Habilizume,W., Hayashida,K., Hayatsu,M., Hiramoto,K., Itoh,W., Kagawa,I., Kanagawa,S., Kach,H., Kawai,J., Kondo,S., Kach,H., Kawai,J., Koha,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nishi,K., Nomura,K., Ninyazaki,A., Murata,M., Nishi,K., Nomura,K., Ninyazaki,A., Murata,M., Nishi,K., Nomura,K., Shinaqawa,A., Shiraki,T., Sakai,C., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Shiraki,T., Tamaki,T., Tamaka,T., Tamaka,T., Waki,K., Tagawa,A., Takahahi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Tayawa,A., Takahahi,F., Tagawa,A., Tayanishi,A., and Mayanizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Nagatu,T., Kawaqashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Obneda,E., Yahaqi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-6602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica
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|mol_type="mRNA"
|cultivar="Nipponbare"
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100.0%; Pred. No. 0.001;
tive 0; Mismatches 0; Indels
                              Science 301 (5631), 376-379 (2003)
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/clone="J033069M07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLPVPI IAEVDLYKLDPWDLPEKALFGRKEWYFFTPRDKYYPDNGSRPNRAAGRGYWKA
TRADEKVAPRYGSARTYGI KKALVYFSGRARGYYTDWINHEYRLADARAPGGKGKGSO
KLDEWVLCRLYNKKWWEKYKLEQQDVASYAAAAPRNHHQNGEWMDAAAADTWSDSF
OTHDSDI DNASAGLRHGGGGGGGGGGGYAPRNGFVTVKEDNDWFTGLNPDELQPPYMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'translation="MAAAVGGSGRRDAEAELNLPPGFRFHPTDEELVVHYLCRKVARQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK073848 1283 bp mRNA linear PLN 24-JUL-2003 Oryza sativa (japonica cultivar-group) cDNA clone:J033069M07, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collection, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK073848.1 GI:32983871
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
2 (bases 1 to 120-7,
Hirano, H.

Hirano, H.

Submitted Submission
Submitted (28-MAY-1999) Hiroyuki Hirano, Univ Tokyo, Graduate
School of Agricultural and Life Sciences; Yayoi 1-1-1, Bunkyo-ku,
Tokyo 113-8657, Japan (E-mail:ahlrano@mail.ecc.u-tokyo.ac.jp,
Tel:+81-3-5841-5065, Eax:+81-3-5641-5063)
Location/Qualifiers
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tive 0; Mismatches
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/note="25 a nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAA89798.1"
/db_xref="G1:6730938"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:4530"
1. .1264
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Best Local S:
Matches 27,
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AK073848/c
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      REFERENCE
AUTHORS
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JOURNAL
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/codon_start=______/codon_start==_____/codon_start==____/codon_start==____/codon_start==____/codon_start==____/codotct====___/case=______/codotct====___/case=_______/codotct===_____/case=________/db__xxef==______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=______/case=_____/case=_____/case=_____/case=_____/case=_____/case=_____/case=_____/case=_____/case=_____/case=_____/case=____/case=____/case=____/case=____/case=____/case=_____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=____/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=___/case=__/case=__/case=__/case=__/case=__/case=__/case=__/case=__/case=__/case=__/ca
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/db_xref="eq1:55762"
/db_xref="eq1:55762"
/db_xref="eq1:55762"
/db_xref="eq1:55762"
/db_xref="eq1:57762"
/db_
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3-KETOACYL-COA THIOLASE PEROXISOMAL"
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STREPDELLENGOTFFRGAYTKULQNISLRRKMLIICKIRSNHWGKKKYTSSTTYSTHL
ATNELAENAHFLDGLVRNLGNISLRKRALVILEKTLRKQSFLQLFLKDEIYLTLIE
KTLPIISKELQFVYLKCFKILMYNPLARIRALHSEBLIRWFTELLTDQNSNIKCQLLS
MELLLLITYVEGSTGCELIMDQLSIIFTDWIEWFDKILADDIAIHSSLYLNMNQLKID
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/note="unnamed protein product; orf, len: 1375, CAI: 0.15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MDSSPNKKTYRYPRRSLSLHARDRVSEARKLEELNLNDGLVAAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="unnamed protein product; orf,len: 235, CAI: 0.15"
                                                                                                                                                                                                                                                                                                                                                                            is given for each CDS.
lambda clones 4357-3717 are between cosmid 9402 and cosmid 8277.
Location/Qualifiers
                                                                                                                                                               Details of the omitted CDS are available on request. The more
significant matches with motifs in the PROSITE database are
also included but some of these may be fortuitous. The length
codons and the calculated codon adaptation index (CAI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="chromosome IX"
/clone="combined sequence of lambda clones 4357-3717"
462. .1169
                              overlapped and those that are overlapped by more than 50% of their length by a larger CDS have been omitted from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="thiolases active site"
complement(1331. .1381)
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/protein_id="CAA86119.1"
/db_xref="G15.57764"
/db_xref="G08.P49450"
/db_xref="SGD:S0001421"
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complement (1220. .2473)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="AB972"
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238059.1 GI:557761
238059.1 GI:557761

238059.1 GI:557762

dina43; dna52; glycerol-3-phosphate dehydrogenase; gut2; human cDNA; limp2; membrane protein; mitochondria aldehyde dehydrogenase; Micochondrial carrier protein; mitochondrial outer membrane protein; molecular chaperone; om45; p23; pantoate-beta-alamine ligase; pot1; rad25; regulatory protein; ray; ribosomal protein; elli, ssl2; sugar utization protein; rcp1-beta; tpm2; tropomyosin; tumor specific transplatation antigen; two component regulatory protein; ubi1; ubiquitin, ubiquitin, ubiquitin, ubiquitin, ubiquitin, zinc
                                                                                                                                                                                                                                                                                                              PAT 22-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katajiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G. Plant genes involved in defense against pathogens
Patent: WO 030080898-A 4864 03-JAN-2003;
Syngenta Participations AG (CH)
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On Oct 3, 2002 this sequence version replaced gi:603997.
Notes:
All CDS over 100 codons have been analysed. CDS that are completely
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 0.001;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                         AAbb4994 2000 bp DNA Sequence 4864 from Patent WO03000898.
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51 AACGCTGCTGCTGCTGCTGCTGCT 77
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Barrell, B. and Rajandream, M.A.
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Matches 27; Conserva
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Query Match

ORIGIN

DEFINITION ACCESSION VERSION

KEYWORDS

RESULT 23 SC4357/c

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LEQRSTSTINENT PERMONITANGAN SILGELEERS STATEMENT STATEME
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IIFQNLAKKQQQQQKISLPKRSTSLLKSKRVTSLSSYLTDANNENESQNBSEDKSKDS
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PTIERSPWTYVSLSITGLRNLGHYCKYKINSM QCL.FAAKTFRTLFISSKKKYLLQPGRANN PTIERSPWTYSLSISKMLRNLGGCSVVPT
YSTTFLLLINSILQGFNNKTALBILNFLKKNNIHNTITFLELAYKDDPNSVVIMEQIK
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/note="unnamed protein product; orf, len: 1071, CAI: 0.13,
some similarity with ubiquitin carboxy terminal
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KVSNNEYKHWFDKNVIGNGISPIDDIFQGQMENSLQCKRCGYTTFNYSTFYVLGLAIP
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LGGSGKRSSSSTPFSTGGNDSNNSSDYKNKKLTTVKTINFVTLPKILVIHLSRFYYDL
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Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y.,
Antonio, B.A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,
Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Arita, K.,
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M. Jiang, J. and Gojobori, T.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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On May 24, 2002 this sequence version replaced gi:16930116.
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BAC clone:OSJNBa0085D07, complete sequence.
                                                                              /note="gut2, len: 649, CAI: 0.19, GPDA YEAST P32191
GLYCEROL 3-PHOSPHATE DEHYDROGENASE, frameshifts with
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Nature 420 (6913), 312-316 (2002)
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-haq 0; Indels
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100.0%; Pred. No. 0.001
...ive 0; Mismatches
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                                                                                                                                                            published sequence"
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AP004331.2 GI:21203157
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COMMENT

gene

seq29-na-truncated.olig10.rge

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/cultivar="Nipponbare"
/db xref="taxon:39947"
/chromosome="1"
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orientation of the sequence is from -21M13 to M13rev of the BAC
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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This sequence was identified as CDM:10210908 by the submitter. For more information on this record e-mail to fly@celera.com.

* NOTE: This is a "working draft" sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                              Gaps
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Madopterygota; Diptera; Brachycera; Muscomorpha;
Phydroida; Drosophilidae; Drosophila.
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                                                                         (japonica cultivar-group) "
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100.0%; Pred. No. 0.0012;
:ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                  5.8%; Score 27; DB 8; Length 88088;
100.0%; Pred. No. 0.0011;
ive 0; Mismatches 0; Indels (
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/organism="Drosophila melanogaster"
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                                                                  /organism="Oryza sativa (...
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cultivar="Nipponbare"
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/clone="OSJNBa0085D07"
                                                                                                                                                                                                                                                                                        51 AACGCTGCTGCTGCTGCTGCTGCT 77
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                                     Location/Qualifiers
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Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,
Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y.,
Antonio, B.A., Kanamori, H., Hosokawa, S., Magukawa, M., Arikawa, K.,
Antonio, B.A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,
Hamada, M., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Arita, K.,
Idonuma, A., Iijima, M., Ikda, S., Honda, M., Itoh, S., Itoh, T.,
Itoh, Y., Itoh, Y., Iwabuchi, A., Kamiya, K., Karasawa, W., Katagiri, S.,
Kikuta, A., Kobayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M.,
Nakama, Y., Nakamichi, Y., Nakaura, M., Namiki, N., Nagishi, M.,
Ohta, I., Ono, M., Saji, S., Sakai, K., Shibata, M., Shimokawa, T.,
Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K.,
Kamagata, H., Yamana, H., Yabilki, S., Yoshihara, R., Yukawa, K.,
Zhong, H., Iwama, H., Endo, T., Ito, H., Hahn, J.H., Kim, H.I., Eun, M.Y.,
Yano, M., Jiang, J. and Gojobori, T.
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AUDITICAL SUBMISSION

AUDITICAL SUBMISSION

Agrobiological Sciences, Rice Genome Research Program; Kannondai

Agrobiological Sciences, Rice Genome Research Program; Kannondai

(E-mail: tsasaki@mias.fffrc.go.ip, URL:http://rgp.dna.affrc.go.jp/,

Tel:81-298-38-7441, Fax:81-298-38-7469)

On Sep 7, 2001 this sequence version replaced gi:14624988.

Genes were predicted from the integrated results of the following:

Genes were predicted from the integrated results of the following:

Genes were predicted from the integrated results of the following:

Genes were predicted from the integrated results of the following:

Gotober 1998 version). The genomic sequence was searched against

NCBI NonRedundant Protein database, net

RGP. Protein homologies of the coding regions were searched against

NCBI NonRedundant Protein database with BLASTP2.0. ESTS represent

RGP. Protein homologies of the coding regions were searched against

NCBI NonRedundant Protein database with BLASTP2.0. ESTS represent

A gene with identity or significant homology to a protein is

corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is

classified based on the protein name to indicate the homology (covering such as same name, 'putative-' and '-like protein'. A gene without as junificant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as a 'hypothetical' protein.

The orientation of the sequence of BIL48D12 clone has an overlap with P0676H03 (DDB3: AP0002385) clone at the position 1 to 45,178 and with P0676H03 and ends at the position 75,992 of P0676H03 and ends at the position 1 to 45,178 and with http://rgp.dna.affrc.go.jp/GenomeSeq.html.

1776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLPVPIIAEVDLYKLDPWDLPEKALFGRKEWYFFTPRDRKYPNGSRPNRAAGRGYWKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (join(1616. .2083,2184. .2470,2569. .2764))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(1616. .2083,2184. .2470,2569. .2764))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The genome sequence and structure of rice chromosome 1 Nature 420 (6913), 312-316 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 132059)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
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gene

CDS

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Complement (join(14359. .14600,14752. .14929,15013. .15084, 15363. .15458,15562. .1578,15760. .15916,16010. .16107, 16100. .16384,16409. .15678,16780. .15916,16010. .16107, 16479. .1566. .17586,17692. .17686,18098. .18909,18297. .18479, 16656. .18757,18857. .18958,19057. .19152,19721. .19798, 18656. .18757,18857. .20179,20275. .20136,0444. .20518, 20625. .208885,20970. .20194,21196. .21571,21368. .21579. .21678,21196. .21574,21196. .21574,21348. .235623,243483. .24487,24596. .24667,24490. .25415,2492. .25577,25644. .25786,26028. .26179,26947. .27060,21163. .27248,27328. .27410,28523. .288587,28664. .28861,28937. .29016,30166. .30289, 30380. .304893,30801)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /traislation="Mrrarceggmwtarglasrwgtsasgsgsglerelgnhanava
TSFLHRHHGSLRWEGGDAKRGNTYVGNAFSSBASMSPRYAPSPSIALPSDPPPAASRV
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RVTASQPNYVRMDSWCEASIRTVVGSTPRODTGGTVYGLSPYTGDRTGGCAPWFHPY
PNGVGAEGYTGLSPVSGGGRRWGPLEDGRLLSFQAKAQIVVRASGCAPWFHPTV
ESKQDDDVRTPRRGEHVEHLGCYYYYGGVREVTVVLSTMHIPRPCCLLNSRTRGPLAAT
GADKPVAPKGSARTVGIKKALVFYSGKAPRGVKTDWIMHEYRLADADRAPGGKKGSQ
                                    KLDEWVLCRLYNKKNNWEKVKLEQQDVASVAAAAPRNHHHQNGEVMDAAAADTMSDSF
QTHDSDIDNASAGIRHGGCGGGGFGDVAPPRNGFVTVKEDNDWFTGLNFDELQPPYYM
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GAKVVPPKKIIKMLPELFDHPDQNVRASSKGLTLELCRWIGKEPVKAIIFEKMRDTMK
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ITDVNLAVSVEATQAIGNLAKGLRTHFSGNSRVLLPVLLEKLKEKKPTWTEALSGTLQ
AMHKSGCITLLDVIEDVRVAVKNKVPLVRSLTLNWVAFCIETSNKATVLKLHKEYVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMSGFSGRFGFSDRQIKKVDYSVTGDQLHVELAWHENFHRWHRRTAAAGGSQPSYVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESQCGRPNTAAGLHGRTVFSRLVAYYYTCSNYCYLRRCSLYVDKCSRTPLPLRKQRVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KELEAELANVSGIAKPTRKIRSEQEKELEEEVVPEAAGTNNSEEAVPEAPMEIDEYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGTEGSFQIDIIPEFGKEMLCRATVVYPVTLINDYELLLARGRIVAFYLDTAIDKPTVM
DSSSMRRSAASMLSGKKPVQAVPATKKSGPAKSATAKKTDGGPQSKASAAPVIEDVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEMSLEEIEEKLSSVVKSETISQLKSTVWKERLEAISMLKQEVESLTELDKSAELLVR
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IGLQSSAAATRNATIKLIGVLHKFVGPDIKGFLSDVKPALLSTLDAEYEKNPFEGTAS
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                                                                                                                                                                                                                                                                                                                          join(6090. .6117,6421. .6572,8325. .8440,8715. .8803,
9502. .9589,9669. .9774,10773. .10866,11020. .11192,
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/gene="mil48012.2"
/note="contains EST
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join(6090. 6317,6421. 6572,8325. 8440,8715. 8803,

9502. 9589,9669. 9774,10773. 10866,11020. 11192,

11536. 111575,12734. 12875,13216. 13303,13676. 13730)

/gene="B114812.2"

join(6090. 6317,6421. 6572,8325. 8440,8715. 8803,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product="putative microtubule associated protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="B1148D12.3"
/note="contains EST C25950(C11258)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein"
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/db_xref="GI:15528780"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHLSGK"
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CDS

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GPADWREALDIVALGLERGOYGEMKTICHELTOANDESSYLDDLIKEADRIVSCHAV
GPADWREALDIVALGLERGOYGEMKTICHELTOANDESSYLDDLIKEADRIVSCHAV
MYFOIKRAHAVKEGTLDNLITELLIMLIDERVPLWDGSQLIKALNVLALKILDNAE
RTSSFVVLINLLRPLDPSRWESPTPEEGLAVKNQKFSDLVWCLIKLTKVLQSTIYEV
DLDRILQSTHIYLQELGWEEIRRAGADDRELRWKTVLHELVKLRGTAIKGHLSMVP
IDABPQPIILAYIDLNLQTLAAARNLTPSGTWGQTHWGDAGSNNPNPSTHSTDAQLKQ
ELAAVFKKGGWGYGTGIGTEIRRITQYPKVDIPPQLQANSERFRYINGAGDAGVEK
NAAGRTBSSLELSTPPPIAPIPSFRANDIPPGLQANGSINNTHGGTREPRGT
LDALRERMKSIQAANGANFDGVQARPLPSWNGNTLHGGTRLDADPQCTQNIIPPMDER
ALSGLQARWERIKSGSMEP."

COMPLEMEN (41340. 43701)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /.3un(46995...47010.47163...47331,48588...48659,48754...48915,
49020...49094,49172...49243,49329...49400,49485...49553,
49972...50106,50186...50655,50730...50888,50981...51120,
51214...51433,51545...51780,51867...52370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .48915,
ADVLKCLGDNKKHMRECTLTALDLWVAAQLDKMVPYITVTLGDQKTGSEGRKDLFDW
LSKTASNMSDPSEALPLIKESASSLADKSSEVRKAAESFWREILKIGGDDVVAKNLKD
LSKTASNMSDPSEALPLIKESASSLADKSSEVRKAAESFWREILKIGGDDVVAKNLKD
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VSQRGIFBARSSVTMISSQDSIGSQALFNISONKEERERRYVKKFFEFERGUDE
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CESNTTCLLKVLDFLPELFDVLKDQSYMLTEAEAAIFLDCLMEKSGHNIEKVREK
                                                                                                                                                                                                                                                                         LIKOMNITYSLPKILPYILEGLRSKNNRTRIECVDIIGYFMDHIGTEVSGILKNILPSV
AALTAERDGEIRKAALNTLATAYKNIGDDVWRYVGKISDAQRSMLDDRFKWKAREMDK
RREGRPGDARAALRRSVRENGSDIAEQSGEAVSRSMAGENFGYSDAHNVPRQMATATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus chromosome 14 clone RP24-201114 map 14, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   jōin(46995. .47010,47163. .4731,48588. .48659,48754. .41
49020. .49094,49172. .49243,49329. .49400,49485. .49553,
49972. .59106,50186. .50655,50730. .50888,50981. .51120,
51214. .51433,51545. .51780,51867. .52370)
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HTG; HTGS_RCLITOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pseudogene
similar to Arabidopsis thaliana chromosome 2, At2g35630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probably inactive due to no termination codon in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative receptor protein kinase"
/protein_id="BAB64823.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 14, clone RP24-201114
Unpublished
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100.0%; Pred. No. 0.00)
--ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="B1148D12.4"
'note="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Annote="Anno
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organism="Mus musculus"

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Cooke, P., DeArellano, K., Deax, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gordt, S., Gayette, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gordt, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illey, T., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lawcoque, K., Landers, T., Lehoczky, J., Marche, R., Liu, G., Macdean, C., Mardonald, P., Major, J., Marquis, N., Mathews, C., Macdean, C., Mardonald, P., Major, J., Marquis, N., Mathews, C., Morman, C.H., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Domell, P., O'Nell, D., O'Connor, T., O'Domell, P., O'Nell, D., Nabord, C., Reterson, K., Phunkang, P., Pierre, N., Pollara, V., Raymond, C., Reterson, K., Phunkang, P., Pierre, N., Pollara, V., Roman, J., Rosetti, M., Spencer, B., Schauer, S., Schueback, R., Stange-Thomann, N., Stojanovic, N., Storery, P., Spencer, B., Stange-Thomann, N., Stojanovic, Viel, R., Vo, A., Wilson, B., Wu, X., Waman, D., Ye, W.J., Young, G., Usumitre, A., Wilson, B., Wu, X., Waman, D., Ye, W.J., Young, G., Direct Submission
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Researl, 320 (Lailer) Edge, Cambringe, rr, 02141, USA

Anderson, N., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,

Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, P., Corum, B., DeArellano, K.,

Diaz, J.S., Doddey, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,

Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,

Graham, L., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, B.,

Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

Lindblad-Toh, K., Liux, Lul, A., Mabbitt, R., Maclean, C.,

Madonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Madonald, P., Major, J., Minova, T., Mlenga, V., Murphy, T., Naylor, J.,

Nguyen, C., Nicol, R., Nioba, C., O'Connor, T., O'Donnell, P.,

Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,

Rachupka, A., Ramasam, U., Raymoni, C., Retta, R., Rise, C., Rogtv, P.,

Roman, J., Schauer, S., Schupback, R., Sewar, S., Severy, P., Smith, C.,

Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M.,

Vassillev, H., Venkataraman, V. S., Viell, R., Vo, A., Wilson, B.,

Nums, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Dec 4, 2003 this sequence version replaced gi:38304329.

All repeats were identified using RepeatMasker:

Smit, A.F. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker:html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

116945 117045 gap of 116945 bp in length 117046 41358: contig of 106 bp
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AC138056 158606 bp DNA linear HTG 09-DEC-2003
Medicago truncatula clone mth2-13i6, WORKING DRAFT SEQUENCE, 3
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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3 (bases 1 to 158606)

Shall, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Direct Submission and Roe, B.A.
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On Dec 9, 2003 this sequence version replaced gi:38502358.
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Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-13i6
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by the finished sequence as soon as it is available and
the accession number will be preserved.

1 103890 103899: gap of unknown length
103890 131370: contrig of 27381 bp in length
13131 131470: contrig of 27381 bp in length
13171 158606: contrig of 27136 bp in length
Location/Qualifiers
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0
                                                                                                                                                                                                                                                                                                                                                           Length 143558;
                                                                                                                                                                                                                                                                                                         Score 27; DB 2; Length 143.
Pred. No. 0.0012;
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The University Of Oklahoma
                                                                                                                           /map="14"
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                                                                                                                                                                                                                                                                                                                                    Query Match 5.8%; Score 27; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 27; Conservative 0; Mismatches
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Medicago truncatula (barrel medic)
Medicago truncatula
/mol_type="genomic DNA"
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/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 GCTGCTGCTGCTGCTGCTGCTTAA 80
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AC138056/c
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/mol_type="genomic DNA"
                 strain="y; cn bw
                                                                                                                                                                                                                                                                                                                                                                                                               27; Conservative
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Estkaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Brikaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bedydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilae; Drosophila.

Scalniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, B.G., Brandon, R.C.,

Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,

Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,

Dodson, K., Dorsett, V., Douple, E., Doyle, C., Dresnek, D., Farfan, D.,

Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,

Gonzalez, M., Hock, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Mosfirefi, A.,

McIntosh, T.C., Moy, M., Murphy, B., Relson, C., Nelson, K.A., Nunoo, J.,

Phouanenavong, S., Pittman, G.S., Patel, S., Pfeiffer, B.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J. C.

Thomilians, A.M., Thanh, J. A.
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Berkeley Drosophila Genome Project
Barkeley Drosophila Genome Project
Barkeley Drosophila Genome Project
Berkeley, CA 94720
This sequence Berkeley outlones of this BAC and its neighboring clones.
Shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster, chromosome X, region 15E-15E, BAC clone BACK15i12, complete sequence.
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Submitted (27-SEP-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Mar 14, 2001 this sequence version replaced gi:7143399.
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Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Clavavez, C., Chew, M., Clastiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Maxda, P., Moshrefi, A.R., Moshrefi, M., Moshrefi, M., Moshrefi, M., Weinburg, T., Zhang, R., Snir, B., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                          Gaps
                               /mol_type="genomic DNA"
/db_xref="taxon:3880"
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/clone_lib="Medicago truncatula BAC library H2"
                                                                                                                                                                                                                                                                                                       ·,
                                                                                                                                                                                                                                     Length 158606;
                                                                                                                                                                                              Score 27; DB 2; Length 1550
Pred. No. 0.0012;
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/mol_type="genomic DNA"
organism="Medicago truncatula"
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100.0%; Pred. No...
0; Mismatches
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Best Local Similarity 100.(
Matches 27, Conservative
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AC010921/c
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP, Information that pi://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by the Recon repeat discovery system (Lurther information see http://www/Projects/D_rerio/fishmask.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL954848 170176 bp DNA linear VRT 23-MAR-2003
Zebrafish DNA sequence from clone CH211-281G7, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cypriniformes; Cyprinidae; Danio.
(bases 1 to 170178)
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/db_xref="taxon:7227"
/db_comesome="X"
/db_comesome="X"
/db_comesome="X"
/map="15E-15E"
/clone="BaCR15L12 (D898)"
/clone="BaCR15L12 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
BBACes.6)
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100.0%; Pred. No. 0.0012;
ive 0; Mismatches 0; Indels 0
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Center: Wellcome Trust Sanger Institute
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Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 CGCTGCTGCTGCTGCTGCTGCTTA 79
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Gaps

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Uppublished

Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission

Submitted (03-DEC-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission

M. Submitted (10-DEC-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

On Dec 10, 2003 this sequence version replaced gi:39228232.
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center
Center Code:UCKNOR
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                    /map="15E-15E"
/clone="BACR06G02 (D1110)"
/clone 11b="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 172332)
Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-6c16
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                                                                                                                                                                                                                                    Length 172069;
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2236: gap of unknown length
4244: contig of 2008 bp in length
4344: gap of unknown length
7875: contig of 3531 bp in length
7975: gap of unknown length
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10848: contig of 2873 bp in length
10948: gap of unknown length
14384: contig of 3436 bp in length
                                                                                                                                                                                                                            5.8%; Score 27; DB 3; I
100.0%; Pred. No. 0.0012;
:ive 0; Mismatches 0;
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Medicago truncatula (barrel medic)
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                                                                                                                                                 pBACe3.6) "
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7976
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RS Gelniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busandon,R.C.,
Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busan,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle C., Dresnek,D., Farfan,D.,
Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy.B., Nelson,C., Nelson,K.A., Nunco,JJ.,
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Noshrefi,A.,
Rapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,
Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
Sequencing of Drosophila chromosome X, region 15E-15E
Unpublished (1998)
Claiker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,B., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Roshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Fulleffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,B.,
Fuller,B., Rom,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
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L Submitted (12-027-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Dec 13, 2001 this sequence version replaced gi:6466928.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                            AC012160 172069 bp DNA linear INV 13-DEC-2001 Drosophila melanogaster, chromosome X, region 15E-15E, BAC clone BACR06G02, complete sequence.
                                                                                                                                                                                             Gaps
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="denomic DNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                5.8%; Score 27; DB 5; I
100.0%; Pred. No. 0.0012;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                   36000 ACGCTGCTGCTGCTGCTGCTGCTT 36026
                                                                                                                                                                                                                                 52 ACGCTGCTGCTGCTGCTGCTT 78
                           /clone="CH211-281G7"
/clone_lib="CHORI-211"
/db_xref="taxon:7955"
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/rpt_family="Alu"
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Direct Submission
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Mus musculus BAC clone RP24-198P16 from chromosome 2, complete
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Subses 1 to 177062)
Direct Submission
Submitted (29-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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Swearengen-Shahid, S., Kozlowicz, A., Boyer, E. and Shahid, S. The sequence of Mus musculus BAC clone RP24-198P16
Unpublished (2001)
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/clone_lib="Medicago truncatula BAC library H2'
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Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0;
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/organism="Medicago truncatula"
/mol_type="genomic DNA"
/db_xref="taxon:3880"
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Unpublished (2001)
3 (bases 1 to 177062)
McPharson, J.D. and Waterston, R.H.
Direct Submission
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AC121924.3 GI:22539273
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Submitted (11-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Aug 29, 2002 this sequence version replaced g1:22476077.
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Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE INFORMATION:
The RECI-24 BAC library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                             This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                      clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is
overlapped by AC112268.
                                                                                                          Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                              /organism="Mus musculus"
mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="RP24-198P16"
clone_lib="RPCI-24"
                                                                                          ---- Genome Center
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/rpt_family="ERV1"
2692. .3019
/rpt_family="MaLR"
4693. .4845
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5183. .5301
/rpt_family="Alu"
5382. .5453
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/rpt_family="ERVK"
228. .1462
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2151. .2375
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1846. .4975
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Loases 1 to 185722)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Browt, A., Calangelo, M., Collins, S., Collymore, A., Cook, A., Colongelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dear, K., Diaz, J.S., Dodge, S., Farro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lakoeque, K., Landarares, R., Landers, T., Lehoczky, J., Levine, R., Matthews, C., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Maclean, C., Maclean, C., Maclean, C., Mardison, P., Marquis, N., Marquis, N., Marthews, C., Norman, C., Senan, S., Severti, M., Roy, A., Santos, R., Schuer, S., Schubback, R., Stange-Thomann, S., Severy, P., Spencer, B., Stange-Thomann, S., Severy, R., Travis, N., Tawis, N., Taw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC102553 18-JUN-200:
Mus musculus clone RP23-159D6, WORKING DRAFT SEQUENCE, 8 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 185722)
Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-159D6
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5.8%; Score 27; DB 10; Length 177062;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
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/rpt family="B2"
complement (44666. .44738)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 AACGCTGCTGCTGCTGCTGCTGCT 77
                  /rpt_family="B2"
3815. 38427
/rpt_family="B2"
38707. 38775
41034. 41175
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41034. 41175
/rpt_family="A175
42647. 43068
                                                                                                                                                                                                                                                                      /rpt_family="B2"
44381. 44438
/rpt_family="ERV1"
44495. 44556
                                                                                                                                                                                                                                                                                                                                  /rruss, .44556
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/4557, .447*
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43072. 44040
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44162. 44313
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2 (bases 1 to 185722)
38110.
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AC102553/c
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[1543]. 15695
[2543]. .15695
[20710. .20873]. .20873
[20710. .20873]. .20874
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31695. 31841
/rpt family="MER1_type"
32462. 32583
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1 32785. 32839
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34169
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14531. 14824
/rpc_family="Alu"
15075. 15141
/rpc_family="RMERIOA"
/rpc_family="RMERIOA"
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/rpc_family="15313
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34095. .34169
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35610. .35998
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10961. .11004
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11283. 11430
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22592. .22806
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23136. .23225
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23456. .23516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family=llD"
2444. 24504
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24653. 24822
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25552. 25755
/rpt_family="B2"
27915. 27973
                                                                  /rpt_family="B2"
7853. 8183
/rpt_family="L1"
8189. .8438
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8439. RAA
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8647__.9273
/rpt_family="L1"
9298__.9577
/rpt_family="B4"
9580__.10116
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8250. .28283
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. .37895
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/rpt_family="B2"
31052. .31177
  1388. 7448
rpt_family="L1"
684. 7851
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family="B2"
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9135.
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3 (bases 1 to 185722)

12 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderball, H.M., Barna, N., Bastien, V., Bloom, T., Badderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Diaz, J.S., Dodgey, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, B., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Najor, J., Peterson, K., Phunkhang, P., Pierre, N., Rachup, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Talamas, J., Taskaya, Ramsamy, U., Raymon, C., Robbs, M., Tavers, M., Vassillev, H., Venkataraman, V. S., Viell, R., Travers, M., Vassillev, H., Venkataraman, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 18, 2003 this sequence version replaced gi:22380811.

All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
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i: gap of 100 bp
t: contig of 667 bp in length
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i: contig of 1897 bp in length
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2 131331: contrig of 61100 bp in length
2 131431: gap of 100 bp
2 185722: contrig of 54291 bp in length.
Location/Qualifiers
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Submitted (25-JUL-2002) Lita Annenberg Hazen Genome Sequencing Submitted (25-JUL-2002) Lita Annenberg Hazen Genome Sequencing Harbor. Vold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA.

On Jul 25, 2002 this sequence version replaced gi:18201769.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROD 25-JUL-2002
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3 (bases 1 to 1888834)
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Genomic sequence for Mus musculus, clone RP23-27007, complete
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                                        /mol_type="genomic DNA"
/db_xref="texton:10090"
clonc="RP21-159D6"
/clone_lib="RPCI-23 Female Mouse BAC"
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100.0%; Pred. No. 0.0012;
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'note="assembly_fragment"
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/note="assembly_fragment"
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vector_side:right"
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Best Local Similarity 100..
Best Local 27, Conservative
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Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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190402 bp DNA linear HTG 15-NOV.
Rattus norvegicus clone CH230-339N2, WORKING DRAFT SEQUENCE, 4
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                                                                                                                                                                                                                                                                                                                            Length 188834;
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assembly was confirmed by restriction digest.
Location/Qualifiers
1..18834
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HTG; HTGS_PHASE1; HTGS_BRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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The Characteristics of Morley, K.C.

E 2 (Dasses I to 190402)

Morley, K.C.

Direct Submission

Submitted (11-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Bouston, TX 77030, USA

3 (Dasses 1 to 190402)

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4 (Molecular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Direct Submission

5 (Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

5 (Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

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5 (Molecular and Human Genetics, Baylor College of Medicine, One Gaylor Plaza, Houston, TX 77030, USA

5 (Molecular and Human Genetics, Baylor College of Medicine, One Mole Gequence on Nov 15, 2002 this sequence version replaced assemble described in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold', Mithin each contig-scaffold, Matchin each contigs are ordered and oriented, and separated may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome table.
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., V. Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, C., Wang, S., Warren, J., Warren, R., Wei, K., Wei, K., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhoo, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Prince, C., G. and Gibbs, R.A.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: Phrap, version 0.990329
Consensus quality: 173476 bases at least Q40
Consensus quality: 175237 bases at least Q30
Consensus quality: 176250 bases at least Q20
Bstimated insert size: 172780; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contect: hgsc.help@bom.tmc.edu/
Contect: hgsc.help@bom.tmc.edu/
Conterproject Information
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/mol_type="genomic DNA'

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misc feature
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Mus musculus clone RP24-216J21, WORKING DRAFT SEQUENCE, 7 unordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 192539)
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o. 0.0012;
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Mus musculus, clone RP24-216J21
Unpublished
                                                                                                                                                                                                                                                                                                          end_sequence:BZ165180"
172198. .173628
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clone_end:T7"
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915. .1432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 GCTGCTGCTGCTGCTGCTGCTTAA 80
                                                                                                                                                                        sequence: BZ165181"
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/note="clone_boundary
clone_end:T7
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Mus musculus (house mouse)
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AC132877
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Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindlad Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthws,C., McCarthy,M.,
Meldrin,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Treafaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-MRR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2003 this sequence version replaced gi:28412043. All repeats were identified using Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert sizē: 191939; sum-of-contigs
Quality coverage: 9.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: L27122
Center clone name: 216 J 21
------ Summary Statistics
Sequencing vector: Plasmid, n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7935: contig of 7935 bp in length 8035: gap of 100 bp 10717: contig of 2682 bp in length 10817: gap of 100 bp 21133: contig of 10016 bp in length 37038: contig of 100 bp 37038: contig of 18625 bp in length 37138: gap of 100 bp 73158: contig of 36220 bp in length 37158: contig of 36220 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
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/note="assembly_fragment"
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/organism="Mus musculus"
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vector_side:left"
8036. _10717
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Mus musculus clone RP23-198G19, WORKING DRAFT SEQUENCE, 6 unordered
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ive 0; Mismatches 0; Indels 0;
                                              37139. 73158 '-
note="assembly_fragment"
73259. 134748
134849. 192539
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/note="assembly_fragment"
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-198G19
                          note="assembly_fragment"
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Mus musculus (house mouse)
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21234.
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Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Maldrim.J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Morbu,C., O'Commor,T., O'Dommell,P.,
Naylor,J., Natol,R., Norbu,C., O'Commor,T., O'Dommell,P.,
Rachupka,A.,Ramasamy,U., Raymon,R., Phunkhang,P., Pierre,N.,
Rachupka,A.,Ramasamy,U., Raymon,G., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schupack,R., Semman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tasafaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viell,R., Vo,A., Wilson,B.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (11-MRA-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 11, 2003 this sequence version replaced gi:24850527.
All repeats were identified using RepeatMasker.
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 117690: contig of 117690 bp in length 1691 117790: gap of 100 bp 118991: contig of 1201 bp in length 18921 contig of 1201 bp in length 1902 129620: contig of 100 bp 1902 129720: gap of 100 bp 17128 147127: contig of 17470 bp in length 17128 14727: gap of 100 bp 1902 186519: contig of 17407 bp in length 1320 186519: contig of 1700 bp 186419: gap of 100 bp 192629: contig of 6210 bp in length 100 2002 192629: contig of 6210 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
Web site: http://www-seg.wi.mit.edu
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119092. .129620
/note="assembly_fragment"
129721. .147127
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/db_xref="taxon:10090"
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission colly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-erranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the rare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Submitted (11-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 1854, WK. E-mail enquirises:

DumqueryGsanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Sequence From the Wouse Genome Sequencing Consortium whole genome Bhotgum may have been used to confirm this sequence. Sequence from the Whole genome shotgum alone has only been used where it has a phred quality of at least 30.

Center: Wellcome Center Confirm this sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL929249 194209 bp DNA linear ROD 21-MAY-2003 Mouse DNA sequence from clone RP23-273G23 on chromosome 2, complete
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
EMBL; Swr, SWISSPROT; Tr: TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-273G23 is from the RPCI-23 Mouse BAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 194209)
                                                                                                                                                                                                                                                                                                                                                     Gaps
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For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
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0
                                                                                                                                                                                                                                                                                         Length 192629;
                                                                                                                                                                                                                                                                            Score 27; DB 2; Length 192
Pred. No. 0.0012;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                144931 CGCTGCTGCTGCTGCTGCTTA 144957
/note="assembly_fragment"
147228...186319-
/note="assembly_fragment"
186420...123629-
/note="assembly_fragment
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1. 194209
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humguery@sanger.ac.uk
                                                                                                                                                                                          vector_side:right"
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                                                                                                                                                                                                                                                                            5.8%; Sco
ilarity 100.0%; Pr
Conservative 0;
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                                                                                                                                                                 clone end:T7
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Best Local Similarity
Matches 27; Conserv
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                                                                                           misc_feature
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JOURNAL
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a PAC.

The sequence was an expensive an expensive and the consent of the clone being a PAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-NOV-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clon Nov 29, 2002 this sequence version replaced gi:25137036. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL845432 195835 bp DNA linear ROD 02-DEC-2002 Mouse DNA sequence from clone RP23-332H19 on chromosome 2, complete
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Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata, Vertebrata, Buteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
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from the RPCI-23 Mouse PAC Library
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For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                             Length 194209;
                                                                                                                                                                                                                      5.8%; Score 27; DB 10; Length 19. 100.0%; Pred. No. 0.0012; ive 0; Mismatches 0; Indels
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/chromosome="%"
/clone="RRP23-273G23"
/clone="lib="RFCI-23"
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Contact: humquery@sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Mammalia; Eutheria; Rodentia;
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Matches 27; Conservative
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AUTHORS
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KEYWORDS
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

REFERENCE

REFERENCE AUTHORS

JOURNAL REFERENCE TITLE JOURNAL

COMMENT

RESULT 41 AC124555

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with colly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the fauture table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; WP., WORMPEP; Information on the WORMPEP databases: can be found at the sequence of the worm of the worm of the sequence of the worm of the sequence of the sequence of the worm of the sequence of the worm of the sequence of the worm of the sequence of 
                                             AL603682 21680 bp DNA linear ROD 24-OCT-2002 Mouse DNA sequence from clone RP23-235J5 on chromosome 11, complete
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                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 211680)
                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (23-OCT-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 25, 2002 this sequence version replaced gi:21952987.
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from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
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100.0%; Pred. No. 0.0012;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25943 AACGCTGCTGCTGCTGCTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: SC
Web Site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/clone_lib="RPCI-23"
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Location/Qualifiers
1. .211680
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Mus musculus
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AL604024
AL604024.7 GI:21211848
HTG.
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Best Local Similarity 100.
Matches 27; Conservative
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                                                                                                           sequence.
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DEFINITION
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JOURNAL
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            AL603682
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Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Brakway, St. Louis, MO 63108, USA
3 (abses 1 to 210174)
Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-JUN-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 210174) Wilson, R.K.
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Submitted (08-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Nov 8, 2003 this sequence version replaced gi:31880269.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 210174)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC124555 210174 bp DNA linear ROD 08-NOV-;
Mus musculus chromosome 14 clone RP23-245K17, complete sequence.
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McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                             51 AACGCTGCTGCTGCTGCTGCTGCT 77
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="14"
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/chromosome="2"
/clone="RP23-332H19"
/clone_lib="RPCI-23"
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Mus musculus
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                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 27; Conservative
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Gaps

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VERSION KEYWORDS

Matches

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ORIGIN

FEATURES

RESULT 42

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Submitted (13-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                         On Sep 13, 2002 this sequence version replaced gi:21105051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
* as soon as it is available and the accession number will
be preserved.
                                                                                                                                                                                                                                                                                                                         Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Bid Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 231829 bases at least Q40
Consensus quality: 231829 bases at least Q30
Consensus quality: 231829 bases at least Q20
Insert size: 213000; agarose-fp
Insert size: 213000; agarose-fp
Insert size: 238015; sum-of-contigs
Quality coverage: 10.72 in Q20 bases; sum-of-contigs
                                                                                                                                            Center: Washington University Genome Sequencing Center
Center code: WUGSC
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of 31206 bp in length
unknown length
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unknown length
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unknown length
of 53114 bp in length
unknown length
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                                                                                                                                                                                                           Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
--------- Project Information --------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 1799 bp in length
gap of unknown length
contig of 1492 bp in length
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unknown length
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                                                                                                                                                                                                                                                                                                                ---- Summary Statistics
          3 (bases 1 to 237094)
McPherson, J.D. and Waterston, R.H.
Direct Submission
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                      Center project name: M_BA0116001
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                           AUTHORS
TITLE
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        REFERENCE
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                                                                                                           COMMENT
                                                                                                                                    Submitted (121-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 25, 2002 this sequence version replaced gi:18477353.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the orresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was completed to the overlapping clone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                           assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, GARLSPROT; Tr:, TREMBL; WP:, WORWPEP; Information on the WORWPEP database can be found at
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Submitted (31-MAR-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-421F23 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus chromosome UNK clone RP23-11601, WORKING DRAFT
SEQUENCE, 16 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0012;
hos 0;
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AC116661.3 GI:22830524
HTG; HTGS_PHASE1; HTGS_PULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Preu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 237094)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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McPherson, J.D. and Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mol_type="genomic DNA'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                               1 (bases 1 to 217278)
Whitehead, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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KEYWORDS
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                                                                                                AUTHORS
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Rattus norvegicus clone CH230-227F3, WORKING DRAFT SEQUENCE, 3
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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HTG, HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                10357. 17265 ...

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17366. 24413 ...

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41865 ...
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5.8%; Score 27; DB 2; I
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                    6585. .10256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AACGCIGCIGCIGCIGCIGCIGCT 77
clone="RP23-11601"
                                                                                                                                                                                                                                                                        vector_side:right"
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                misc_feature
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BGBHA.A. ESCOUTEON, ENGENE, C., FVAILS, T., FRANG, G.
FERNBAGEA, S., FAILBY, M., FLAGG, N., FORDES, L., FOSTER, P., FARSER, C. M., Gantal, M., FOSTER, P., Garcia, A., Garner, T., Garrar, M., Handler, P., Hawes, A., Handler, M., Hamilton, C., Hamilton, K., Harlar, M., Harlar, M., Handler, M., Harlar, M., Harlar, M., Harlar, M., Garkson, A., Garkson, A., Garkson, J., Jackson, L., Jang, H., Johnson, B., Ghas, M., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Marzhin, S., Kelly, S., Kelly, S., Khan, Z., Khan, Z., Liu, Y., Liu, Y., London, P., Lorgacre, S., Lopez, J., Liu, Y., Loulsedd, H., Johnson, B., Mari, M., Martin, M., Marrin, M., Mahindartne, M., Mahindartne, M., Mahindartne, M., Mahindartne, M., Mahindartne, M., Mahindartne, M., Manguw, B., Mullosavijevic, A., Mine, G., Munidasa, M., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Morris, S., Mallos, M., Morris, S., Mullosavijevic, A., Mine, G., Manja, M., Morris, S., Manja, M., Morris, S., Manja, D., Newton, N., Nguyen, N., Norris, S., Paul, M., Perez, A., Perez, M., Perez, M., Pelak, S., Paul, M., Perez, M., Reser, R., Rish, M., Morris, S., Reeves, R., Rish, S., Paul, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Bhen, H., Sanders, M., Solerty, G., Shatsman, S., Shen, H., Shetty, G., Shvatsheby, A., Sisson, I., Streng, K., Warten, W., Walker, B., Wang, C., Warten, W., Walse, K., Warten, V., Vallas, R., Walse, M., Walse, K., Walse, M., Wa
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Submitted (13-MMY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23606053.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bmc.imc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas sassembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Direct Submission
Submitted (16-AUG-2002) Human Geneme Sequencing Center, Department of Modecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 237312)
Rat Genome Sequencing Consortium.
Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine
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Web site: http://www.hgsc.bcm.tmc.edu/

Center code: BCM

COMMENT

seq29-na-truncated.olig10.rge

32

Page

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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240501 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-132D18, WORKING DRAFT SEQUENCE, 2
unocaced pieces.
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HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus
Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Assembly program: Atlas 3.0;
Consensus quality: 201099 bases at least Q40
Consensus quality: 207416 bases at least Q30
Consensus quality: 2107456 bases at least Q30
Estimated insert size: 213682; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                     63260: contig of 63260 bp in length 63360: gap of unknown length 235896: contig of 17236 bp in length 235996: gap of unknown length 237332: contig of 1336 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0012;
0.0012;
0. Indels
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tive 0; Mismatches
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8193. 8812
'note="ollone boundary
clone end:T7
site:EcoRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              end_sequence:BZ104008"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           654. .1459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                63261
63361
235897
235997
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AC099207/c
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Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cookrell,R., Cox.C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draph,H., Divya,K., Eggan,A., Bacetto,M., Faggy,N., Forbee,I., Foster,M., Foster,P., Faster,C.M., Ganza,M., Garcia,A., Garcia,A., Garcia,A., Garcia,M., Garcia,M., Garcia,M., Garcia,M., Ganza,M., Gabrer,T., Faster,C.M., Gabis,M., Hall,R., Gardia,A., Garcia,A., Garcia,M., Karpathy,S., Kelly,S., Kally,S., Martin,K.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             And Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (Dases 1 to 240501)

RS Bat Genome Sequencing Consortium.

Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:25095914.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, and separated by sized gaps filled with No to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Unpublished
2 (bases 1 to 240501)
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Direct Submission
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TITLE
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Web site: http://www.hgsc.bcm.tmc.edu/

Center code: BCM

COMMENT

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AUTHORS
TITLE
JOURNAL
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Allen, H., Alebrooke, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alebrooke, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyadi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D. 'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Durn, A., Durbin, K., Duval, B., Baves, K.,
Erane, K., Bscotto, M., Eugene, C., Evans, C., A., Falls, T., Far, G.,
Fernandez, S., Finley, M., Flagen, C., Aver, Falls, T., Foster, P.,
Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garra, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC129456 240561 bp DNA linear HTG 13-NOV-2002 Rattus norvegicus clone CH230-9K8, WORKING DRAFT SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                        Consensus quality: 227593 bases at least Q40 consensus quality: 227593 bases at least Q30 consensus quality: 229405 bases at least Q30 consensus quality: 230440 bases at least Q30 Estimated insert size: 236821; sum-of-contigs estimation quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1238878: contig of 238878 bp in length 8879 238978: gap of unknown length 8979 240501: contig of 1523 bp in length. Location/Qualifiers

1. 240501

/ organism="Rattus norvegicus" / mol_type="genomic DNA" / mol_type="genomic DNA" / clone="CH230-132D18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC129456.5 GI:24940997
HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47005 AACGCTGCTGCTGCTGCTGCTGCT 46979
                                                                                    Center clone name: CH230-132D18
                  Center project Information
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                Assembly program: Atlas 3.0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 AACGCTGCTGCTGCTGCTGCTGCT 77
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238879
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AC129456/c
LOCUS
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Gunaratue, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Hanland, W., Hamil, C., Hamilton, C., Hamilton, K., Hannang, Y., Harland, P., Hisaban, M., Handand, M., Hannang, M., Harland, M., Hannang, R., Misaban, R., Joliver, A., Gacdeni, L., Rand, M., Ghulton, B., Channang, M., Dolina, B., Gacdeni, L., Rand, M., Ghulton, B., Channang, M., Dolina, G., Kand, L., Kand, M., Mannand, M., Ma
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Submitted (26-AUG-2001) Whitehead Institute/MIT Center for Genome
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Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46051: contig of 46051 bp in length
46151: gap of 100 bp
48744: contig of 2593 bp in length
16844: gap of 100 bp
168635: contig of 119791 bp in length
168735: gap of 100 bp
242978: contig of 74243 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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100.0%; Pred. No. 0.0012;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIBR
Web site: http://www-seg.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="RP23-61L24"
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Best Local Similarity
Matches 27; Conserve
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46152
48745
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168636
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JOURNAL
                                                 TITLE
JOURNAL
                                                                                                                       REFERENCE
AUTHORS
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2 (bases 1 to 242978)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chasgro, B., Choepel, Y., Colargelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Firzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Galagan, L., Garnd-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lakocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., Maclara, C., Macdonald, P., Major, J., Marquis, M., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Maldrim, J., Nahova, T., Major, J., Whyphy, T., Naylor, J., Nguyen, C., Norman, C.H.K., Phunkhang, P., Pierre, N., Pollara, V., Oliver, J., Peeterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Sewery, P., Spencer, B., Stange-Thomann, N., Schupback, N., Strauge-Thomann, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces of the gaps between them are solven, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1. (bases 1 to 242978)
       Estimated insert size: 218439; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                        by the finished sequence as soon as it is available and the accession number will be preserved.

1 240561: contig of 240561 bp in length.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC093480 242978 bp DNA linear
Mus musculus chromosome 13 clone RP23-61L24 map 13,
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HTG; HTGS PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 13, clone RP23-61L24
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/mol type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136293 GCTGCTGCTGCTGCTGCTTTAA 136267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 GCTGCTGCTGCTGCTGCTTAA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238534. .240561
/note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="wgs contig"
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Gaps

seq29-na-truncated.olig10.rge

AC125723

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clone_end:Sp6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Namany, D.Marie, Wetzker, M.Lee, Abramzon, S., Adams, C., Allen, E., Allen, H., Alsbrooks, S., Amin, A. Angulano, D., Anyale, W. Baraker, M. Baca, E., Baden, H., Baldaria, S., Baldaria, S., Baldaria, B., Baldaria, B., Baldaria, J., Blankerburg, K., Blyth, P., Brown, M., Benalmed, F., Biswalo, K., Blart, J., Blankenburg, K., Blyth, P., Brown, M., Benalmed, F., Biswalo, K., Blart, J., Blankenburg, K., Blyth, P., Brown, M., Calderon, B., Cardenas, V., Carer, K., Calderon, B., Cardenas, V., Carer, K., Chen, Z., Chen, Y., Colleron, B., Chen, Z., Cheer, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Cher, Z., Chen, Z.
                                                                                                                                          ACL25723 250546 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-6D11, WORKING DRAFT SEQUENCE, 2
unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
199395 AAGGTGCTGCTGCTGCTGCTGCT 199421
                                                                                                                                                                                                                                                            AC125723 GI:30467499
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2 (bases 1 to 250546)
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TITLE
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Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:24818284.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.lcm.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
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NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: Atlas;

Consensus quality: 223239 bases at least Q40
Consensus quality: 226328 bases at least Q30
Consensus quality: 228344 bases at least Q20
Estimated insert size: 233947; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 250546)
Rat Genome Sequencing Consortium.

Direct Submission
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Center clone name: CH230-6D11
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/note="wgs end_extension
clone_end:T7"
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186843. .227017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marzhy, Dandare, Marzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Avogaja, A., Ayodeji, M., Baca, E., Baden, H., Balabrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Dandaranake, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blayth, P., Brown, M., Baldvin, D., Bandaranake, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blayt, C., Burch, P., Burnell, K., Caldaron, E., Carter, M., Carter, M., Carter, M., Carter, M., Candaron, E., Cardenas, V., Carter, C., Coryel, M., Cree, A., D'Gouza, L., Davila, M., L., Davis, C., Darsmo, C., Coyle, N., Dinh, T., Chu, J., Caparon, E., Cardenas, V., Carter, M., Davila, M., Escotto, M., Garter, M., Garter, T., Garza, M., Garratte, P., Hadland, M., Hamil, C., Hamilton, C., Hamiton, K., Harvey, Y., Haviak, P., Hawes, A., Hander, M., Hamilton, C., Hamiton, K., Harvey, T., Haviak, P., Halland, M., Hamil, C., Hamilton, C., Hamiton, K., Martin, K., Marti
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                                                                                                                                                                                                                                                                                                                                            AC128474 258061 bp DNA linear HTG 21-SEP-2002 Rattus norvegicus clone CH230-51A3, *** SEQUENCING IN PROGRESS ***.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                          5.8%; Score 27; DB 2; Length 250546;
100.0%; Pred. No. 0.0012;
iive 0; Mismatches 0; Indels 0;
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HTGS, HTGS, PHASE2; HTGS DRAFT, HTGS_ENRICHED.
Rattus norvegicus
Rattus norvegicus
                                                                                                                                                                            14787 GCTGCTGCTGCTGCTGCTTAA 14813
                                                                                                                                              54 GCTGCTGCTGCTGCTGCTTAA 80
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DEFINITION
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AC128474
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TITLE

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.
                                                                                                                                                                                                                                                                Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 21, 2002 this sequence version replaced gi:21909191.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequency reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                       Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Contact: hgsc-help@bcm.tmc.edu
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256785. .258061
/note="wgs_end_extension
clone_end:Sp6"
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Rat Genome Sequencing Consortium
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note="clone_boundary"
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2 (bases 1 to 258061)
Worley, K.C.
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Query Match 5.8%; Score 27; DB 2; Length 258061; Best Local Similarity 100.0%; Pred. No. 0.0012; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: May 25, 2004, 18:30:57 Job time : 3357 secs